

STIC-Biotech/ChemLib

124324

From: Kaushal, Sumesh
Sent: Thursday, June 10, 2004 10:41 AM
To: STIC-Biotech/ChemLib
Subject: 09734672: Interference and Sequence search

mej

09734672: Interference and Sequence search

Please search

- SEQ ID NO:3 1-5711 DNA
- SEQ ID NO:3 120-5708 DNA.

Thanks

S. Kaushal

AU1636, REM2.B85

Ph: 571-27-20769

Mail Box: REM2.C70

- Enpn, Enpn each file removed - SK

RECEIVED
JUN 10 2PM
(610)

Searcher: _____
Phone: _____
Location: _____
Date Picked Up: *6/10/04*
Date Completed: _____
Searcher Prep/Review: _____
Clerical: _____
Online time: _____

TYPE OF SEARCH: ☒
NA Sequences: _____
AA Sequences: _____
Structures: _____
Bibliographic: _____
Litigation: _____
Full text: _____
Patent Family: _____
Other: _____

VENDOR/COST (where applic.)
STN: _____
DIALOG: _____
Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: *01/04*
WWW/Internet: _____
Other (specify): _____

GenCore version 5.1.6
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OK nucleic - nucleic search, using sw model

Run on: June 11, 2004, 17:45:31 ; Search time 12866 Seconds
(without alignments)
12972.154 Million cell updates/sec

Title: US-09-734-672A-3_COPY_120_5708

Perfect score: 5589

Sequence: 1 ATGGATTATCTGCTCTTCG.....AGATCCCCACAGCCACTAC 5589

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: em_estba:*

2: em_esthum:*

3: em_estm:*

4: em_estm:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_hc:*

9: gb_est1:*

10: gb_est2:*

11: gb_hc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_ptg:*

27: em_gss_vxl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1960.8	35.1	2101	11	BC012577 Homo sapi
2	1955	35.0	2090	11	BC030969 Homo sapi
3	1416.4	25.3	1578	11	BC038947 Homo sapi
4	941	16.8	1919	11	AK086173 Mus muscu

5	863	15.4	962	13	BQ068830
6	841.4	15.1	1089	12	BM452288
7	811.8	14.5	845	9	AUI22476
8	760.2	13.6	783	9	AUI42729
9	750.6	13.4	789	14	CK000353
10	746.4	13.4	933	13	BUI71200
11	738.8	13.2	743	12	BG681276
12	701.2	12.5	739	14	CF121736
13	688	12.3	702	9	AUI25312
14	686.6	12.3	739	10	BF508987
15	686.4	12.3	987	12	BM600251
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19	619.4	11.1	856	13	BUI47444
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45	498.2	8.9	509	10	AW504244

ALIGNMENTS

RESULT 1	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.	2101 bp	mRNA	linear	HTC 04-MAR-2003
LOCUS	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.				
DEFINITION	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.				
ACCESSION	BC012577.1	GI:15214876				
VERSION	BC012577.1	GI:15214876				
KEYWORDS	HTC.					
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
REFERENCE	1	(bases 1 to 2101)				
AUTHORS	Strausberg R.					
TITLE	Direct Submission					
JOURNAL	Submitted (15-AUG-2001) National Institutes of Health, Mammalian					
	Gene Collection (MGC), Cancer Genomics Office, National Cancer					
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,					
	USA					
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov					
COMMENT	Contact: MGC help desk					
	Email: cgapbs-remail.nih.gov					
	Tissue Procurement: ATCC					
	CDNA Library Preparation: CLONTECH Laboratories, Inc.					
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)					
	DNA Sequencing by: Institute for Systems Biology					
	http://www.systemsbio.org					
	contact: amadan@systemsbiology.org					

Anup Madan, Jessica Fahey, Erin Helton, Mark Ketterman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAL Plate: 19 Row: a Column: 18
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 6552298
This clone has the following problem: retained intron.

FEATURES

Location/Qualifiers

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/clone="IMAGE:3996659"
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ORIGIN

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Matches 1965; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

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Qy 181  TGTCCTTTATGTAGAATGTATACCAAAAGGAGCCCTACAGAAAGTACCAGATTTAGT 240
Db 304 TGTCCTTTATGTAGAATGTATACCAAAAGGAGCCCTACAGAAAGTACCAGATTTAGT 363

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Qy 361  GAACTTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCAGAAAGACTTCTACAGAT 420
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Qy 421  GAACCCGAAAATCTCTTCCTTCAGGAAACCGAGTCTCAGTGTCCAACTCTCTAAACCTTGA 480
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Qy 1801  CACAATTCAAAAACACCTTAAAAAGATAGGCTGAGGAGGAGGATCTCTTCTTACAGGCATATT 1860

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Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S.,
Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A.,
Muramatsu, M. and Hayashizaki, Y.
Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of
Physical and Chemical Research (RIKEN), Laboratory for Genome
Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222,
Fax: 81-45-503-9216)
cDNA library was prepared and sequenced in Mouse Genome
Encyclopedia project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in RIKEN,
Division of Experimental Animal Research in Riken contributed to
prepare mouse tissues.
Please visit our web site for further details.
URL: http://genome.gsc.riken.go.jp/
URL: http://fantom.gsc.riken.go.jp/.

FEATURES
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Matches 1343; Conservative 0; Mismatches 363; Indels 113; Gaps 7;
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ORGANISM   Homo sapiens
REFERENCE  1 (bases 1 to 962)
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT    Contact: Robert Strausberg, Ph.D.
           Email: cgapbs@mail.nih.gov
           Tissue Procurement: ARCC
           cDNA Library Preparation: Rubin Laboratory
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           Clone distribution: MGC clone distribution information can be
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               California, Berkeley) using ZAP-cDNA synthesis kit
               (Stratagene) and Superscript II RT (Life Technologies).
               Note: this is a NIH_MGC Library."
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Db      15 TTGGCAGCAGGCACATCAGAAAGACAGTATTAACCTTCACAGAAAGTAGTGAAATACCC 74
Qy      4392 TATAAGCCAGAAATCCAGAAAGGCCCTTCTCTGCTGACAAAGTTTGAGGTCTCTGACATAGTTC 4451
Db      75 TATAAGCCAGAAATCCAGAAAGGCCCTTCTCTGCTGACAAAGTTTGAGGTCTCTGACATAGTTC 134
Qy      4452 TACCAGTAAATAAAGAAACCAAGAGTGTGAAGAGTCTATCCCTTTCTAAATGCCCACATTT 4511
Db      135 TACCAGTAAATAAAGAAACCAAGAGTGTGAAGAGTCTATCCCTTTCTAAATGCCCACATTT 194
Qy      4512 AGATGATAGTGTGTATCATGCACAGTTGCTCTGGGAGTCTTTCAGAAATAGAAACCTACCCATC 4571
Db      195 AGATGATAGTGTGTATCATGCACAGTTGCTCTGGGAGTCTTTCAGAAATAGAAACCTACCCATC 254
Qy      4572 TCAAGAGGAGCTCATTAAGGTTTGTATGTGAGGAGCAACAGCTCGAAGAGTCTGGGCC 4631
Db      255 TCAAGAGGAGCTCATTAAGGTTTGTATGTGAGGAGCAACAGCTCGAAGAGTCTGGGCC 314
Qy      4632 ACACGATTTGACGGAACATCTTACTTTCAGAGGCAAGATCTAGAGGGAACCCCTTACCT 4691
Db      315 ACACGATTTGACGGAACATCTTACTTTCAGAGGCAAGATCTAGAGGGAACCCCTTACCT 374
Qy      4692 GGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAACTCTGATCTTCTGAAGACAGAGC 4751
Db      375 GGAATCTGGAATCAGCCTCTTCTCTGATGACCCCTGAACTCTGATCTTCTGAAGACAGAGC 434
Qy      4752 CCAGAGTCTGCTGTGTTGGCAACATACCATCTTCAACCTCTGCAATGAAAGTCCCA 4811
Db      435 CCAGAGTCTGCTGTGTTGGCAACATACCATCTTCAACCTCTGCAATGAAAGTCCCA 494
Qy      4812 ATTTGAAAGTTGCAAGATCTGCCAGGTCAGCTGCTGCTCATCTACTGATATCTGCTGG 4871
Db      495 ATTTGAAAGTTGCAAGATCTGCCAGGTCAGCTGCTGCTCATCTACTGATATCTGCTGG 554
Qy      4872 GTATAATGCAATGAAAGAAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4931
Db      555 TTATAATGCAATGAAAGAAAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 614
Qy      4932 AAGGTCACAAAGAAAGTGTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 4991
Db      615 AAGGTCACAAAGAAAGTGTGCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 674
Qy      4992 CGTGTACAAAGTTTCCAGAGAAACACCAATCATCTTTAACTTAATCTGAAGAGAC 5051
Db      675 CGTGTACAAAGTTTCCAGAGAAACACCAATCATCTTTAACTTAATCTGAAGAGAC 734
Qy      5052 TACTCATGTTTATGAGAAACAGATGCTGAGTTTGTGTGAGAACGGACACTGAAATATTT 5111
Db      735 TACTCATGTTTATGAGAAACAGATGCTGAGTTTGTGTGAGAACGGACACTGAAATATTT 794
Qy      5112 TCTAGCAATTCGGGAGGAGAAATGGGTAGTCTAGTCTATTTCTGGGTGACCCAGTCTATTAA 5171
Db      795 TCTAGCAATTCGGGAGGAGAAATGGGTAGTCTAGTCTATTTCTGGGTGACCCAGTCTATTAA 854
Qy      5172 AGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGAGG--TCAATGGA 5229
Db      855 AGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGAGGTCATATGGA 914
Qy      5230 AGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGAGGTCATATGGA 5254
Db      915 AGAAAGAAATGCTGAAATGAGCATGATTTTGAAGTCAGAGGAGATGAGGTCATATGGA 939

RESULT 6
BQ452288
LOCUS      6386302 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:5526666
DEFINITION 5', mRNA sequence.
ACCESSION BQ452288
VERSION    BQ452288.1 GI:18501328
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

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Best Local Similarity 99.1%; Pred. No. 2e-169;
Matches 836; Conservative 0; Mismatches 5; Indels 3; Gaps 2;

QY 3700 GTAAACAAATACCTTCTCAGTCTACTAGCATAAGCACCGCTTCTACCGAGTCTGTCT 3759
Db 1 GTAAACAAATACCTTCTCAGTCTACTAGCATAAGCACCGCTTCTACCGAGTCTGTCT 60

QY 3760 AAGAACACAGAGAGAGATTTATATCATTCGAAGATAGCTTAATGACTCAGTCAACCCAG 3819
Db 61 AAGAACACAGAGAGAGATTTATATCATTCGAAGATAGCTTAATGACTCAGTCAACCCAG 120

QY 3820 GTAATATTTGCAAGGCACTCTCAGGACATCAGCTTAGTGAGGAAACAAATGTTCTGCT 3879
Db 121 GTAATATTTGCAAGGCACTCTCAGGACATCAGCTTAGTGAGGAAACAAATGTTCTGCT 180

QY 3880 AGCTGTGTTCTTCAAGTCAGTGAATTTGGAAGATAGCTTAATGACTCAGTCAACCCAG 3939
Db 181 AGCTGTGTTCTTCAAGTCAGTGAATTTGGAAGATAGCTTAATGACTCAGTCAACCCAG 240

QY 3940 GATCCTTTCTGATGTTCTTCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 3999
Db 241 GATCCTTTCTGATGTTCTTCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 300

QY 4000 GGTCGTAGTCAAGGAAATTTGTTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAA 4059
Db 301 GGTCGTAGTCAAGGAAATTTGTTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAA 360

QY 4060 AATAATCAAGAGAGAGCAAGTGAATTTCAATGTTGAGTGAAGCAGCATCTGGGTGTGAG 4119
Db 361 AATAATCAAGAGAGAGCAAGTGAATTTCAATGTTGAGTGAAGCAGCATCTGGGTGTGAG 420

QY 4120 AGTGAAACAAAGCGTCTCTGAAGACTGCTCAGGCTATTCCTCTCAGAGTGAATTTAAAC 4179
Db 421 AGTGAAACAAAGCGTCTCTGAAGACTGCTCAGGCTATTCCTCTCAGAGTGAATTTAAAC 480

QY 4180 ACTCAGCAGAGGATACCATGCAACATGCTGAAGCTTCTAACAGCTTACCCCTTCCATCAT 4239
Db 481 ACTCAGCAGAGGATACCATGCAACATGCTGAAGCTTCTAACAGCTTACCCCTTCCATCAT 540

QY 4240 CTAGAAGCTGTGTAGAACAGCAGTGGGAGCGAGCTTCTAACAGCTTACCCCTTCCATCAT 4299
Db 541 CTAGAAGCTGTGTAGAACAGCAGTGGGAGCGAGCTTCTAACAGCTTACCCCTTCCATCAT 600

QY 4300 AGTGACTTCTTCTGCGCTTGAAGACTCTCGAAATTCAGAACAAAGCAATCAGAAAGCA 4359
Db 601 AGTGACTTCTTCTGCGCTTGAAGACTCTCGAAATTCAGAACAAAGCAATCAGAAAGCA 660

QY 4360 GTATTAACTTCAAGAAAGTAGTGAATACCTTAAGCCAGAAATCCAGAGGCTTTCT 4419
Db 661 GTATTAACTTCAAGAAAGTAGTGAATACCTTAAGCCAGAAATCCAGAGGCTTTCT 720

QY 4420 GCTGACAAAGTTGAGGTGTCTGAGATAGTTCTTACCAAGTAAATTAAGAACCAAGGA -G 4477
Db 721 GCTGACAAAGTTGAGGTGTCTGAGATAGTTCTTACCAAGTAAATTAAGAACCAAGGAAGT 780

QY 4478 TGGAAAGGTCA-TCCCTTCTTAATGCGCATCATAGATGATAGTGTGATCAGTCAAGT 4536
Db 781 TGGAAAGGTCA-TCCCTTCTTAATGCGCATCATAGATGATAGTGTGATCAGTCAAGT 840

QY 4537 TGCT 4540
Db 841 TGCT 844

RESULT 8
AUI42729
LOCUS
DEFINITION AUI42729 Y79A1 Homo sapiens cDNA clone Y79A1000792 5', mRNA
sequence.
ACCESSION AUI42729
VERSION AUI42729.1 GI:11004250
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 783)
AUTHORS Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saiko, K., Kawai, Y., Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and Isogai, T.
TITLE HRI human cDNA project
JOURNAL Unpublished (2000)
COMMENT Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
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Location/Qualifiers
1..783
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/db_xref="taxon:9606"
/clone="Y79A1000792"
/cell_type="retinoblastoma"
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/clone_lib="Y79A1"
/note="Vector: pME18SPL3"

ORIGIN
Query Match 13.6%; Score 760.2; DB 9; Length 783;
Best Local Similarity 99.1%; Pred. No. 5.6e-158;
Matches 773; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 3460 TTAGATGATGGTGAATAAAGGAAGATAGTCTGCTGTAATAATCAGATTTAGGAAAGT 3519
Db 1 TTAGATGATGGTGAATAAAGGAAGATAGTCTGCTGTAATAATCAGATTTAGGAAAGT 60

QY 3520 TCTGCTGTTTTAGCAAAAAGCGTCCAGAGAGAGAGCTTTAGCAGGAGTCTAGCCCTTTC 3579
Db 61 TCTGCTGTTTTAGCAAAAAGCGTCCAGAGAGAGAGCTTTAGCAGGAGTCTAGCCCTTTC 120

QY 3580 ACCATACACATTTGGCTCAGGTTTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAA 3639
Db 121 ACCATACACATTTGGCTCAGGTTTACCGAAGAGGGGCCAAGAAATAGAGTCTCAGAA 180

QY 3640 GAGAACTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCCAAACACTTGTATTGGTAA 3699
Db 181 GAGAACTTATCTAGTGAGGATGAAGAGCTTCCCTGCTTCCAAACACTTGTATTGGTAA 240

QY 3700 GTAACAATATACCTTCTCAGTCTACTAGGCAATAGCACCGTGTCTACCGAGTCTGTCT 3759
Db 241 GTAACAATATACCTTCTCAGTCTACTAGGCAATAGCACCGTGTCTACCGAGTCTGTCT 300

QY 3760 AAGAACACAGAGAGAGATTTATATCATTCGAAGATAGCTTAATGACTCAGTCAACCCAG 3819
Db 301 AAGAACACAGAGAGAGATTTATATCATTCGAAGATAGCTTAATGACTCAGTCAACCCAG 360

QY 3820 GTAATATTTGCAAGGCACTCTCAGGACATCAGCTTAGTGAGGAAACAAATGTTCTGCT 3879
Db 361 GTAATATTTGCAAGGCACTCTCAGGACATCAGCTTAGTGAGGAAACAAATGTTCTGCT 420

QY 3880 AGCTGTGTTCTTCAAGTCAGTGAATTTGGAAGATAGCTTAATGACTCAGTCAACCCAG 3939
Db 421 AGCTGTGTTCTTCAAGTCAGTGAATTTGGAAGATAGCTTAATGACTCAGTCAACCCAG 480

QY 3940 GATCCTTTCTGATGTTCTTCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 3999
Db 481 GATCCTTTCTGATGTTCTTCCAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTT 540

QY 4000 GGTCGTAGTCAAGGAAATTTGTTTCAGATGATGAAGAAAGAGAAACGGGCTTGAAGAA 4059

Tissue Procurement: AFCC/DCTD/DTF
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM13514 row: C column: 21
 High quality sequence stop: 672.

FEATURES
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6161612"
 /tissue_type="melanotic melanoma"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_72"
 /notes="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 2 kb. Library constructed by Life
 Technologies."

ORIGIN
 Query Match 13.4%; Score 746.4; DB 13; Length 933;
 Best Local Similarity 98.3%; Pred. No. 6.8e-155;
 Matches 765; Conservative 0; Mismatches 11; Indels 2; Gaps 1;

Qy 4590 GGTGTTGATGTGAGGAGCAACAGCTGGAGAGTCTGGGCCACACGATTTCAGCGAATC 4649
 Db 12 GGTGTTGATGTGAGGAGCAACAGCTGGAGAGTCTGGGCCACACGATTTCAGCGAATC 71

Qy 4650 ATCTTACTTCCAGGCAAGATCTAGAGGAAACCCCTTACTTGGAAATCTGGAATCAGCCT 4709
 Db 72 ATCTTACTTCCAGGCAAGATCTAGAGGAAACCCCTTACTTGGAAATCTGGAATCAGCCT 131

Qy 4710 CTCTCTGATGACCTGAATCTGATCTCTTGAAGCAGAGCCCGAGTCTGCTGTG 4769
 Db 132 CTCTCTGATGACCTGAATCTGATCTCTTGAAGCAGAGCCCGAGTCTGCTGTG 191

Qy 4770 TGGCAACATACCTCTTCAACCTCTGCAATGAAAGTTCCCAATGAAAGTTGCAAGATC 4829
 Db 192 TGGCAACATACCTCTTCAACCTCTGCAATGAAAGTTCCCAATGAAAGTTGCAAGATC 251

Qy 4830 TGCCAGGCTCAGCTCTGCTGATCTACTGATCTGCTGGGTATATCAATCTGAGAG 4889
 Db 252 TGCCAGGCTCAGCTCTGCTGATCTACTGATCTGCTGGGTATATCAATCTGAGAG 311

Qy 4890 AAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4949
 Db 312 AAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371

Qy 4950 GTCCATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 5009
 Db 372 GTCCATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 431

Qy 5010 AAAACACCATCATCTTTAACTAATCTAATCTAATCTAATCTAATCTAATCTAATCTAATCT 5069
 Db 432 AAAACACCATCATCTTTAACTAATCTAATCTAATCTAATCTAATCTAATCTAATCTAAT 491

Qy 5070 AACAGATGCTGAGTTGTGTGTGTAACGGACACTGAAATATTTTCTAGGAATTCGGGAGG 5129
 Db 492 AACAGATGCTGAGTTGTGTGTGTAACGGACACTGAAATATTTTCTAGGAATTCGGGAGG 551

Qy 5130 AAAATGGGTAGTTAGCTATTCTGGGTGACCCAGTCTATTAAAGAAAGAAATGCTGAA 5189
 Db 552 AAAATGGGTAGTTAGCTATTCTGGGTGACCCAGTCTATTAAAGAAAGAAATGCTGAA 611

Qy 5190 TGACATGATTTTGAAGTCAGAGGAGATGTGGTCAATGGAGAAACCAACCAAGTCCAAA 5249
 Db 612 TGACATGATTTTGAAGTCAGAGGAGATGTGGTCAATGGAGAAACCAACCAAGTCCAAA 671

Qy 5250 GCGAGCAAGAGATCCAGGAGCAGAAAGATCTTCAGGGGGCTAGAAATCTGTGCTATGG 5309

Db 672 GCGAGCAAGAGATCCAGGAGCAGAAAGATCTTCAGGGGGCTAGAAATCTGTGCTATGG 731

Qy 5310 GGCCTTACCACATGCCCCAG--ATCACTGGATGGATGGATGGATGGATGGATGGATGG 5365

Db 732 GGCCTTACCACATGCCCCAGGATGGATGGATGGATGGATGGATGGATGGATGGATGG 789

RESULT 11
 BG681276 743 bp mRNA linear EST 01-MAY-2001
 LOCUS 602627125F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751887 5',
 DEFINITION mRNA sequence.
 ACCESSION BG681276
 VERSION BG681276.1 GI:13912673
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 743)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail@nih.gov
 Tissue Procurement: James Cleaver, M.D.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 cDNA Library Arrayed by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM10609 row: a column: 08
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FEATURES
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 /clone="IMAGE:4751887"
 /tissue_type="squamous cell carcinoma"
 /lab_host="DH10B (T1 phage-resistant)"
 /clone_lib="NCI CGAP Skn4"
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 Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.
 Average insert size 1.5kb. Library constructed by Life
 Technologies. Note: this is a NCI_CGAP Library."

ORIGIN
 Query Match 13.2%; Score 738.8; DB 12; Length 743;
 Best Local Similarity 99.7%; Pred. No. 3.2e-153;
 Matches 740; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4605 GAGCAACAGCTGGAGAGTCTGGGCCACACGATTTCAGCGAATCTTCTGATGACCC 4664
 Db 1 GAGCAACAGCTGGAGAGTCTGGGCCACACGATTTCAGCGAATCTTCTGATGACCC 60

Qy 4665 GCAAGATCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 4724
 Db 61 GCAAGATCTAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 120

Qy 4725 TGAATCTGATCTCTTGAAGACAGAGCCCGAGTCTGCTGTGTTGGCAACATCAATC 4784
 Db 121 TGAATCTGATCTCTTGAAGACAGAGCCCGAGTCTGCTGTGTTGGCAACATCAATC 180

Qy 4785 TTCAACTCTGATTTGAAGATTTCCCAATTTGAAGTTGAGATCTGCCCGGTCAGC 4844
 Db 181 TTCAACTCTGATTTGAAGATTTCCCAATTTGAAGTTGAGATCTGCCCGGTCAGC 240

Qy 4845 TGCCTGCTCATCTACTGATCTGCTGGGTATATGCAATGGAGAGAGTGTGAGCGAGGA 4904
 Db 241 TGCCTGCTCATCTACTGATCTGCTGGGTATATGCAATGGAGAGAGTGTGAGCGAGGA 300


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QY 4905 GAAGCCAGAAATTGACAGCTTCAACAGAAAGGTCACAAAGAAATGTCCATGTTGGTGTC 4964
Db |||||||
QY 301 GAAGCCAGAAATTGACAGCTTCAACAGAAAGGTCACAAAGAAATGTCCATGTTGGTGTC 360
Db |||||||
QY 4965 TGGCCTGACCCCAAGAGAAATTTATGCTCGTGACAGTTTGCAGAAAACACCAACATCAC 5024
Db |||||||
QY 361 TGGCCTGACCCCAAGAGAAATTTATGCTCGTGACAGTTTGCAGAAAACACCAACATCAC 420
Db |||||||
QY 5025 TTTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 5084
Db |||||||
QY 421 TTTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACTAACT 480
Db |||||||
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Db |||||||
QY 481 TGTGTGTGAACGACACTGAAATATTTTCTAGGAATTTGCGGAGGAAATGCGGTAGTTAG 540
Db |||||||
QY 5145 CTATTTCTGGGTGACCCAGCTGCTATTAAGAAAGAAATGCTGAATGAGCATGCTGAGTT 5204
Db |||||||
QY 541 CTATTTCTGGGTGACCCAGCTGCTATTAAGAAAGAAATGCTGAATGAGCATGCTGAGTT 600
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QY 5205 AGTCAGAGGAGATGCTGCTCAATGGAAGAAACCAACAGGCTCCAAAGCGAGCAAGAAATC 5264
Db |||||||
QY 601 AGTCAGAGGAGATGCTGCTCAATGGAAGAAACCAACAGGCTCCAAAGCGAGCAAGAAATC 660
Db |||||||
QY 5265 CCAGGACAGAAAGATCTTCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCACCAACAT 5324
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QY 661 CCAGGACAGAAAGATCTTCAGGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCACCAACAT 720
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QY 5325 GCCCAGACATCAACTGGAATGG 5346
Db |||||||
QY 721 GCCCAGACATCAACTGGAATGG 742
Db |||||||
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RESULT 12
CF121736
LOCUS
DEFINITION
UI-HF-BP0p-arm-q-04-0-UI.r1.NIH.MGC_51 Homo sapiens cDNA clone
IMAGE:30566859 5', mRNA sequence.
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ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 739)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
8889548
Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEBRP, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Louis Staudt
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5, Location/Qualifiers
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/mol_type="mRNA"
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/clone="IMAGE:30566859"
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FEATURES

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/notes="Vector: pT7T3-Pac; Site_1: NotI; Site_2: Eco RI;
Constructed from size fractionated cytoplasmic mRNA
(4.4-7.4kb). Directionally cloned. Cells provided by
Louis M. Staudt, Ph.D. Library preparation by Maria de
Patima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."
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ORIGIN

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Query Match 12.5%; Score 701.2; DB 14; Length 739;
Best Local Similarity 98.0%; Pred. No. 7.2e-145;
Matches 720; Conservative 0; Mismatches 14; Indels 1; Gaps 1;
QY 2233 GAAGACCCCAAGATCTCATGTTAACTGGAGAAAGGGTTTGCAAACTGAAAGATCTGTA 2292
Db 6 GGAGACCCCAAGATCTCATGTTAACTGGAGAAAGGGTTTGCAAACTGAAAG-TCTGTA 64
QY 2293 GAGAGTAGCAGTATTTCACTCTGTTACTGATTATGGCACTCAGGAAAGTATCTCG 2352
Db 65 GAGAGTAGCAGTATTTCACTCTGTTACTGATTATGGCACTCAGGAAAGTATCTCG 124
QY 2353 TTACTGGAGTTAGCACTCTAGGGAGGCAAAAACAGAACCAATAAATGTGTGAGTCAG 2412
Db 125 TTACTGGAGTTAGCACTCTAGGGAGGCAAAAACAGAACCAATAAATGTGTGAGTCAG 184
QY 2413 TGTGACAGCATTTGAAACCCCAAGGACATAATTCATGTTGTTCCAAAGATATAGAAAT 2472
Db 185 TGTGACAGCATTTGAAACCCCAAGGACATAATTCATGTTGTTCCAAAGATATAGAAAT 244
QY 2473 GACACAGAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAACCAAGTCGGGAAACAGC 2532
Db 245 GACACAGAGGCTTTAAAGTATCCATTTGGGACATGAAGTTAACCAAGTCGGGAAACAGC 304
QY 2533 ATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTCCAGAAATACATTCAGAGTTTCA 2592
Db 305 ATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTCCAGAAATACATTCAGAGTTTCA 364
QY 2593 AAGCGCAGTCATTTGCTCTGTTTTCATATCCAGGAAATGCGAGAGGAAATGTGCAACA 2652
Db 365 AAGCGCAGTCATTTGCTCTGTTTTCATATCCAGGAAATGCGAGAGGAAATGTGCAACA 424
QY 2653 TTCTCTGCCACCTCTGGGTCCTTTAAAGAAACCAAAAGTCCAAAAGTCACTTTTGAATGTGA 2712
Db 425 TTCTCTGCCACCTCTGGGTCCTTTAAAGAAACCAAAAGTCCAAAAGTCACTTTTGAATGTGA 484
QY 2713 CAAAAGGAGAAATCAAGGAAAGATGATCTTAATATCAGCCTCTACAGAGTATAT 2772
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QY 2773 ATCACTGCAAGGCTTTCTGTTGTTGTCAGAAAGATAAGCCAGTTGATATGCAAAATGT 2832
Db 545 ATCACTGCAAGGCTTTCTGTTGTTGTCAGAAAGATAAGCCAGTTGATATGCAAAATGT 604
QY 2833 AGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCAACGAAATCTGA 2892
Db 605 AGTATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCAACGAAATCTGA 664
QY 2893 CTCATTACTCCAAATAAACAATGAGCTTTTACAAAACCCATATCGTATACCAACCACTTTT 2952
Db 665 CTCATTACTCCAAATAAACAATGAGCTTTTACAAAACCCATATCGTATACCAACCACTTTT 724
QY 2953 CCCATCAAGTCAATTT 2967
Db 725 TCCATCAAGTCAATTT 739
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sequence.
ACCESSION      AUI25312.1 GI:10950028
VERSION
SOURCE         EST.
ORGANISM       Homo sapiens (human)
REFERENCE      1 (bases 1 to 702)
AUTHORS       Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S. and Isogai, T.
TITLE         HRI human cDNA project (Ota, T., Wakamatsu, A., Ozawa, M., Ishii, S., Saito, K., Yamamoto, J., Nakamura, Y., Nishikawa, T., Nagai, T., Suzuki, Y., Sugano, S., Isogai, T.)
JOURNAL        Unpublished (2000)
COMMENT       Contact: Takao Isogai
               Genomics Laboratory
               Helix Research Institute
               1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
               Tel: 81-438-52-3975
               Fax: 81-438-52-3986
               Email: genomics@hri.co.jp
               HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
               Research Institute; cDNA library construction: Department of
               Virology, Institute of Medical Science, University of Tokyo, and
               Helix Research Institute.
FEATURES       source
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Best Local Similarity 99.4%; Pred. No. 6.1e-142;
Matches 699; Conservative 0; Mismatches 3; Indels 1; Gaps 1;
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LOCUS
DEFINITION
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VERSION
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SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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BF508987
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EST.
Homo sapiens (human)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
The sequence contained an oligo-dT track that was present in the
oligonucleotide that was used to prime the synthesis of first
strand cDNA and therefore this may represent a bonafide poly A
tail. cDNA Library Preparation: M.B. Soares Lab Clone distribution:
NCI-CGAP clone distribution information can be found through the
I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/bbrp/image/image.html
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/note="Vector: pT73D-Pac (Pharmacia) with a modified
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is a subcloned library derived from NCI CGAP Sub5. The
NCI CGAP Sub8 library had 2.5 million recombinants. A
single-stranded DNA preparation of NCI CGAP Sub5 was used
as a tracer in a subtractive hybridization with a driver
comprising: a pool of clones from NCI CGAP Sub5 (IMAGE
clone ids 2732833-2737415, 3068040-3069191, 25% of the
driver population), a pool of clones from NCI CGAP Sub4
(IMAGE clone ids 2723592-2729326, 25% of the driver
population), NCI CGAP Sub6 (pool A19-AJU, IMAGE ids
2728969-2733190, 25% of the driver population), and
NCI CGAP Sub7 (IMAGE ids 3069192-3072238,
3081864-3084550, 25% of the driver population).
Subtraction was performed as previously described
[Bonaldo, Lennon & Soares (1996): Normalization and
Subtraction: Two Approaches To Facilitate Gene Discovery.
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Genome Research 6, 791-806.
TAG_SEQ=None found"

ORIGIN

Query Match 12.3%; Score 686.6; DB 10; Length 739;
Best Local Similarity 99.1%; Pred. No. 1.3e-141;
Matches 689; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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RESULT 15
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BM800251
VERSION
BM800251.1 GI:19117074
KEYWORDS
EST.
ORGANISM
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 987)
NIH-MGC <http://mgc.nci.nih.gov/>
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
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Location/Qualifiers

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ORIGIN

Query Match 12.3%; Score 686.4; DB 12; Length 987;
Best Local Similarity 85.8%; Pred. No. 1.5e-141;
Matches 874; Conservative 0; Mismatches 14; Indels 131; Gaps 5;
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DB 238 TCAAAAGACGTCTGTCTACATTTGAATTTGGATCTGATTTCTTCTGAGATACCGTTAATA 264
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Job time : 12875 secs

GenCore version 5.1.6
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Run on: June 11, 2004, 17:57:55 ; Search time 336 Seconds
(without alignments)
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Scoring table: IDENTITY_NUC

Gapop 10.0 , Capext 1.0

Searched: 582709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents NA:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1
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; Sequence 5, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antonette C.
; APPLICANT: Alvarez, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ONCORMED
; STREET: 200 Perry Parkway
; CITY: Gaithersburg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,691
FILING DATE: 12-Feb-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Gallegos
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: PA-0054CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2051
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRAINEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17

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Sequence 4, Appl
Sequence 10, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 12, Appl
Sequence 6, Appl
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Db		3240	TCAAAGCAATATTAAATGAGTAGTGGTTCCAGTACTAATCAAGTGGGCTCCAGTATTTAATGAA	3299

Qy	3181	ATAGGTTCCAGTGAAGAAAACATTC	CAAGCAGAACTAGGTAGAGAAA	CHAGGGCCAAATTTG	3240	
Db	3300	ATAGGTTCCAGTGAAGAAAACATTC	CAAGCAGAACTAGGTAGAGAAA	CHAGGGCCAAATTTG	3359	
Qy	3241	AATGCTATGCTTGAATTAGGGGTTTT	GCAACCTGAGGCTCTATAA	CAAAAGTCTTCTCTGA	3300	
Db	3360	AATGCTATGCTTGAATTAGGGGTTTT	GCAACCTGAGGCTCTATAA	CAAAAGTCTTCTCTGA	3419	
Qy	3301	AGTAATTGTAAAGCATCTGAAATTA	AAAAAGCAAGAAATATGA	AGAAAGTAGTTCAGACTGTT	3360	
Db	3420	AGTAATTGTAAAGCATCTGAAATTA	AAAAAGCAAGAAATATGA	AGAAAGTAGTTCAGACTGTT	3479	
Qy	3361	AATACAGATTTCTCCATCTGATTT	CAGATTAATCTTAGAACACGCT	ATATGCGAAGTAGCT	3420	
Db	3480	AATACAGATTTCTCCATCTGATTT	CAGATTAATCTTAGAACACGCT	ATATGCGAAGTAGCT	3539	
Qy	3421	CATGCATCTCAGGTTTGTCTCGACA	CACTGTAGACCTGTTAGATGAT	GGTGAATAAAG	3480	
Db	3540	CATGCATCTCAGGTTTGTCTCGACA	CACTGTAGACCTGTTAGATGAT	GGTGAATAAAG	3599	
Qy	3481	GAAGATCTAGTTTGTCTGAAATATG	CAATTAGGAAAGTTCTGCTGTT	TTTATGCAAAAGC	3540	
Db	3600	GAAGATCTAGTTTGTCTGAAATATG	CAATTAGGAAAGTTCTGCTGTT	TTTATGCAAAAGC	3659	
Qy	3541	GTCCAGAGAGCAGCTTTACGAGAGT	CTCTAGCCCTTTACCCATACACAT	TTTGGCTCAG	3600	
Db	3660	GTCCAGAGAGCAGCTTTACGAGAGT	CTCTAGCCCTTTACCCATACACAT	TTTGGCTCAG	3719	
Qy	3601	GGTTACCGAGAGGGGCAAGAAATTA	GAGTCTCAGAGAGAACTTA	TCTAGTGAGAT	3660	
Db	3720	GGTTACCGAGAGGGGCAAGAAATTA	GAGTCTCAGAGAGAACTTA	TCTAGTGAGAT	3779	
Qy	3661	GAGAGCTTCCCTGCTTCCAACTGTT	ATTGTTGTAAGTAAACAATA	TACCTTCTCAG	3720	
Db	3780	GAGAGCTTCCCTGCTTCCAACTGTT	ATTGTTGTAAGTAAACAATA	TACCTTCTCAG	3839	
Qy	3721	TCTACTAGGCATAGCACCGTTGCT	ACGAGTGTCTGTTAAGAAACA	CAGAGGAGAAATTA	3780	
Db	3840	TCTACTAGGCATAGCACCGTTGCT	ACGAGTGTCTGTTAAGAAACA	CAGAGGAGAAATTA	3899	
Qy	3781	TTATCATTTGAGATAGCTTAATATG	CTGCAGTAAACCCAGGTAA	TATTTGGCAAAAGGATCT	3840	
Db	3900	TTATCATTTGAGATAGCTTAATATG	CTGCAGTAAACCCAGGTAA	TATTTGGCAAAAGGATCT	3959	
Qy	3841	CAGAAACATCACCTTAGTGAAGAAA	CAAAATGTTCTGCTAGCTGTT	TTCTTCAAGTGC	3900	
Db	3960	CAGAAACATCACCTTAGTGAAGAAA	CAAAATGTTCTGCTAGCTGTT	TTCTTCAAGTGC	4019	
Qy	3901	AGTGAAATTGGAAGACTTGA	CTGCGAAATACAAACCCAGGAT	CCCTTCTTGATTGTTCT	3960	
Db	4020	AGTGAAATTGGAAGACTTGA	CTGCGAAATACAAACCCAGGAT	CCCTTCTTGATTGTTCT	4079	
Qy	3961	TCCAAAACAAATGAGGCATCAGT	CTGAAAGCCAGGGAGTTG	TCTGAGTGA	CAAGGAATG	4020
Db	4080	TCCAAAACAAATGAGGCATCAGT	CTGAAAGCCAGGGAGTTG	TCTGAGTGA	CAAGGAATG	4139
Qy	4021	GTTCAGATGATGAAGAAAGAGGA	ACGGGCTTGGAGAAAATAT	TAATCAGAGAGCAAGC	4080	
Db	4140	GTTCAGATGATGAAGAAAGAGGA	ACGGGCTTGGAGAAAATAT	TAATCAGAGAGCAAGC	4199	
Qy	4081	ATGGATTCAAACTTAGGTGAAGCAG	CACTCGGGTGTGAGAGTCAAA	CAAGCGTCTCTGAA	4140	
Db	4200	ATGGATTCAAACTTAGGTGAAGCAG	CACTCGGGTGTGAGAGTCAAA	CAAGCGTCTCTGAA	4259	
Qy	4141	GACTGCTCAGGGCTATCTCTCAGAG	TGAACAATTTTAAACCTCAG	CAGAGGATACCATG	4200	
Db	4260	GACTGCTCAGGGCTATCTCTCAGAG	TGAACAATTTTAAACCTCAG	CAGAGGATACCATG	4319	
Qy	4201	CAACATAACCTGATATAAGCTCC	ACGAGAAATGCGTAACTAGA	AGCTGTGTTAGAACAG	4260	
Db	4320	CAACATAACCTGATATAAGCTCC	ACGAGAAATGCGTAACTAGA	AGCTGTGTTAGAACAG	4379	
Qy	4261	CATGGGAGCCAGCCCTTCTAA	CAGCTACCCCTTCCATCA	TAAAGTGA	CTTTTGGCCCTTGAG	4320

QY 4381 AGTGAATACCCCTATACCCAGGATCCAGAGGCGCTTTCTGCTGACAAAGTTGAGGTGCT 4440
DB 4500 AGTGAATACCCCTATACCCAGGATCCAGAGGCGCTTTCTGCTGACAAAGTTGAGGTGCT 4559
QY 4441 GCAGATAGTTCTACCAAGTAAATAAAGAACCCAGGAGTGAAGAGTCTCCCTCTTAA 4500
DB 4560 GCAGATAGTTCTACCAAGTAAATAAAGAACCCAGGAGTGAAGAGTCTCCCTCTTAA 4619
QY 4501 TGCCCATCATTAGATGATAGTGGTATCATGACAGTTGCTCTGGAGTCTTTCAGATAGA 4560
DB 4620 TGCCCATCATTAGATGATAGTGGTATCATGACAGTTGCTCTGGAGTCTTTCAGATAGA 4679
QY 4561 AACTACCCATCTCAGAGGAGCTCATTAAAGTTGTTGATGTGAGGAGCAACAGCTGGAA 4620
DB 4680 AACTACCCATCTCAGAGGAGCTCATTAAAGTTGTTGATGTGAGGAGCAACAGCTGGAA 4739
QY 4621 GAGTCTGGGCGCACACGATTTGACGGAACAATCTTACTTGGCCAAAGGCAAGATCTAGAGGA 4680
DB 4740 GAGTCTGGGCGCACACGATTTGACGGAACAATCTTACTTGGCCAAAGGCAAGATCTAGAGGA 4799
QY 4681 ACCCTTACCTGGAATCTGGAATCAGCTCTCTCTGATGACCTGAACTGATCTCTTCT 4740
DB 4800 ACCCTTACCTGGAATCTGGAATCAGCTCTCTCTGATGACCTGAACTGATCTCTTCT 4859
QY 4741 GAAGACAGAGCCCGACAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATG 4800
DB 4860 GAAGACAGAGCCCGACAGTCTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATG 4919
QY 4801 AAAGTTCCCGCAATGAAGTTGAGATCTGCCAGGTCAGCTGCTGCTGCTGCTGCTGCT 4860
DB 4920 AAAGTTCCCGCAATGAAGTTGAGATCTGCCAGGTCAGCTGCTGCTGCTGCTGCTGCT 4979
QY 4861 GATACCTGCTGGTATATGCAATGGAAGAAAGTGTGAGGAGGAGGAGGAGGAGGAGGAG 4920
DB 4980 GATACCTGCTGGTATATGCAATGGAAGAAAGTGTGAGGAGGAGGAGGAGGAGGAGGAG 5039
QY 4921 GCTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 4980
DB 5040 GCTTCAACAGAAAGGTCACAAAGAAATGTCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 5099
QY 4981 GAATTTATGCTGCTGATCAAGTTGCGCAGAAACACCAATCACTTAACTAACTAACT 5040
DB 5100 GAATTTATGCTGCTGATCAAGTTGCGCAGAAACACCAATCACTTAACTAACTAACT 5159
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DB 5160 ACTGAAGAGACTACTCATGTTGTTATGAACAGATGCTGAGTTGTTGTTGTTGTTGTTGTT 5219
QY 5101 CTGAATATTTCTGAGAAATGCGGAGGAAATGCTGAGTTGTTGTTGTTGTTGTTGTTGTTG 5160
DB 5220 CTGAATATTTCTGAGAAATGCGGAGGAAATGCTGAGTTGTTGTTGTTGTTGTTGTTGTTG 5279
QY 5161 CAGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTGAAGTCAGAGGAGATGTTG 5220
DB 5280 CAGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTGAAGTCAGAGGAGATGTTG 5339
QY 5221 GTCAATGGAAGAAACCAAGGTCGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5280
DB 5340 GTCAATGGAAGAAACCAAGGTCGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5399
QY 5281 TTCAGGGGGCTAGAAATCTGTTGCTATGGGCGCTTACCAACATGCCAGGAGTCAACTG 5340
DB 5400 TTCAGGGGGCTAGAAATCTGTTGCTATGGGCGCTTACCAACATGCCAGGAGTCAACTG 5459
QY 5341 GAATGAGTGTACAGCTGTGTGGTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5400
DB 5460 GAATGAGTGTACAGCTGTGTGGTCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5519
QY 5401 GGCACAGGTGTCCACCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5460
DB 5520 GGCACAGGTGTCCACCAATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 5579

QY 5461 TTCCATGCAATTGGCCAGATGTGTGAGGCACTGTGTGAGCCGAGAGTGGGTGTGGAC 5520
DB 5580 TTCCATGCAATTGGCCAGATGTGTGAGGCACTGTGTGAGCCGAGAGTGGGTGTGGAC 5639
QY 5521 AGTGTAGCACTTACCAAGTCCAGGAGTGTGACACCTGATACCTGATACCTGATACCTG 5580
DB 5640 AGTGTAGCACTTACCAAGTCCAGGAGTGTGACACCTGATACCTGATACCTGATACCTG 5699
QY 5581 AGCCACTAC 5589
DB 5700 AGCCACTAC 5708

RESULT 3
US-09-074-476-3
Sequence 3, Application US/09074476
Patent No. 6130322
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: Allen, Antonette C.
APPLICANT: Alvares, Christopher P.
APPLICANT: Critz, Brenda S.
APPLICANT: Olson, Sheri J.
APPLICANT: Thurber, Denise
APPLICANT: Zheng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
TITLE OF INVENTION: BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSER: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Homo sapiens
STRAIN: BRCA1 (om12)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-09-074-476-3

Query Match 100.0%; Score 5589; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGAGTTATCTGCTCTTCGCGTTGAGAAAGTACAAATATCTATTATGCTATCGAAA 60
DB 120 ATGGAATATATCTGCTCTTCGCGTTGAGAAAGTACAAATATCTATTATGCTATCGAAA 179
QY 61 ATCTTAGAGTGTCCATCTCTGTCTGAGCTTGATCAAGAACTGTCTCCACAAAGTGTGAC 120
DB 180 ATCTTAGAGTGTCCATCTCTGTCTGAGCTTGATCAAGAACTGTCTCCACAAAGTGTGAC 239
QY 121 CACATATTTGCAAAATTTGCTGCTGAACTTCTCAACAGAAAGAGGCTTCCACAG 180
DB 240 CACATATTTGCAAAATTTGCTGCTGAACTTCTCAACAGAAAGAGGCTTCCACAG 299
QY 181 TGTCTTTATGTAAGATGATATAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGT 240
DB 300 TGTCTTTATGTAAGATGATATAACCAAAAGAGGCTTCAAGAAAGTACGAGATTAGT 359
QY 241 CAACCTGTGAGAGCTATTTGAAATCATTTTGTCTCTTTTCAAGCTTGACACAGTTTGGAG 300
DB 360 CAACCTGTGAGAGCTATTTGAAATCATTTTGTCTCTTTTCAAGCTTGACACAGTTTGGAG 419
QY 301 TATGCAACAGCTATAATTTTGCAAAAGAGAAATTAACCTCTCTGAAACATCTAAAGAT 360
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QY 361 GAACTTTCTATCATCAAAAGTATGGCTTACAGAAACCGTGCCTGCAAAAGACTTCTACAGAT 420
DB 480 GAACTTTCTATCATCAAAAGTATGGCTTACAGAAACCGTGCCTGCAAAAGACTTCTACAGAT 539
QY 421 GAAACCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTACCTTGA 480
DB 540 GAAACCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTACCTTGA 599
QY 481 ACTGTGAACTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTACCTTGA 540
DB 600 ACTGTGAACTCTGAGGAAACAGCTCTCAGTGTCCAACTCTCTACCTTGA 659
QY 541 GAACTGGGATCTGATTTCTGAAATACCCCTCAAGCAACCGGATGAAATCAGTTTGGATTCT 600
DB 660 GAACTGGGATCTGATTTCTGAAATACCCCTCAAGCAACCGGATGAAATCAGTTTGGATTCT 719
QY 601 GATCAAGAAATTTTACAAATCAACCTCAAGCAACCGGATGAAATCAGTTTGGATTCT 660
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QY 661 GCACAAAAGGCTGTGTGAAATTTTCTGAGAGCGGATGAAATCAGTTTGGATTCT 720
DB 780 GCACAAAAGGCTGTGTGAAATTTTCTGAGAGCGGATGAAATCAGTTTGGATTCT 839
QY 721 CCCAGTAAATATGATTTGAAACCACTGAGAGCGGATGAAATCAGTTTGGATTCT 780
DB 840 CCCAGTAAATATGATTTGAAACCACTGAGAGCGGATGAAATCAGTTTGGATTCT 899
QY 781 TATCAGGCTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCC 840
DB 900 TATCAGGCTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCAAAATCTCATGCC 959
QY 841 AGCTCATATCAGCATGAGAAACAGAGTTTATTTACTCTATTAAGACAGATGAAATGAGAA 900
DB 960 AGCTCATATCAGCATGAGAAACAGAGTTTATTTACTCTATTAAGACAGATGAAATGAGAA 1019
QY 901 AAGGCTGAAATCTGTAATAAAGCAACAGCTGCTGCTTACGAGAGCCACATTAACAGA 960
DB 1020 AAGGCTGAAATCTGTAATAAAGCAACAGCTGCTGCTTACGAGAGCCACATTAACAGA 1079
QY 961 TGGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGATCTCCAGCAGCAAGAAAGGTA 1020
DB 1080 TGGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGATCTCCAGCAGCAAGAAAGGTA 1139
QY 1021 GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAAATGAAATGAAATGAAATGAA 1080
DB 1140 GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGAAATGAAATGAAATGAAATGAA 1199
QY 1081 TCAGAGAAATCCTAGAGATATCTGAAGATGTTCTTGGATTAACACTAAATAGCAGCATTCAG 1140

DB 1200 TCAGAGAAATCCTAGAGATATCTGAAGATGTTCTCTGATAAACACTAAATAGCAGCATTCAG 1259
QY 1141 AAAGTTAATGATGTTTTCAGAAAGTATGAACTTCTAGTGTCTGATGACTCACAATGAT 1200
DB 1260 AAAGTTAATGATGTTTTCAGAAAGTATGAACTTCTAGTGTCTGATGACTCACAATGAT 1319
QY 1201 GGGGAGTCTGAATCAAAATGCCAAAGTATGATGATTAATGGAAGTCTTAAATGAGGTAGAT 1260
DB 1320 GGGGAGTCTGAATCAAAATGCCAAAGTATGATGATTAATGGAAGTCTTAAATGAGGTAGAT 1379
QY 1261 GAATATTTCTGGTTCTTCAGAGAAATATAGACTTATCTGAGCAGTATCTCTCATGAGGCTTTA 1320
DB 1380 GAATATTTCTGGTTCTTCAGAGAAATATAGACTTATCTGAGCAGTATCTCTCATGAGGCTTTA 1439
QY 1321 ATATGTAAAGTGAAGAGTTCACCTCCAATCAGTAGAGAGTAATATTTGAAGACAAAATA 1380
DB 1440 ATATGTAAAGTGAAGAGTTCACCTCCAATCAGTAGAGAGTAATATTTGAAGACAAAATA 1499
QY 1381 TTTGGAAACCTATTCGGAAGAGGCAAGCTTCCCAACTTAAGCCATGTAACTGAAAT 1440
DB 1500 TTTGGAAACCTATTCGGAAGAGGCAAGCTTCCCAACTTAAGCCATGTAACTGAAAT 1559
QY 1441 CTATATTTAGGAGCAATTTCTGAGCCACAGATTAATCAAGAGGCTCCCTCACAAT 1500
DB 1560 CTATATTTAGGAGCAATTTCTGAGCCACAGATTAATCAAGAGGCTCCCTCACAAT 1619
QY 1501 AAATTTAAAGCGTAAAGAGGACCTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAA 1560
DB 1620 AAATTTAAAGCGTAAAGAGGACCTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAA 1679
QY 1561 GCAGATTTGGCAGTTCAAAAGAGCTCTGAAATGATTAATCAAGGAACTTAACCAAAAGGAG 1620
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QY 1621 CAGATTTGCTCACTGATGATTAATTTACTAATAGTGGTCTAGAGAAATTAACCAAAAGGAT 1680
DB 1740 CAGATTTGCTCACTGATGATTAATTTACTAATAGTGGTCTAGAGAAATTAACCAAAAGGAT 1799
QY 1681 TCTATTTCAAGATGAGAAATCTTAACCAATAGATCACTCGAAAGAAATCTGCTTTC 1740
DB 1800 TCTATTTCAAGATGAGAAATCTTAACCAATAGATCACTCGAAAGAAATCTGCTTTC 1859
QY 1741 AAACGAAAGCTCAACTTAAGCAGCAGTATTAAGCAATATGAACTCGAAATTAATATC 1800
DB 1860 AAACGAAAGCTCAACTTAAGCAGCAGTATTAAGCAATATGAACTCGAAATTAATATC 1919
QY 1801 CACATTTCAAAAGCACTTAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATTT 1860
DB 1920 CACATTTCAAAAGCACTTAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGCAATTT 1979
QY 1861 CATTGCTTGAATCTAGTGTAGTAAATCTTAAGCCCACTTAATTTGTACTGAAATTCAA 1920
DB 1980 CATTGCTTGAATCTAGTGTAGTAAATCTTAAGCCCACTTAATTTGTACTGAAATTCAA 2039
QY 1921 ATTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAGAAAGTACAAACCAATGCCAGTC 1980
DB 2040 ATTGATAGTTGTTCTAGCAGTGAAGAGATTAAGAAAGAAAGTACAAACCAATGCCAGTC 2099
QY 1981 AGGCACAGCGAAACCTTCAACTCTATGGAAGGTAAGAACTCTGCACTGAGGCGCAGAG 2040
DB 2100 AGGCACAGCGAAACCTTCAACTCTATGGAAGGTAAGAACTCTGCACTGAGGCGCAGAG 2159
QY 2041 AGTAACAGCCAAATGAACAGAAAGTAAAGAAAGTACAGCAGTGTATCTTTCCAGAGCTG 2100
DB 2160 AGTAACAGCCAAATGAACAGAAAGTAAAGAAAGTACAGCAGTGTATCTTTCCAGAGCTG 2219
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QY 2161 TTTGCTCAATCTAGCTTCCAGAGGAAAGAAAGAGAGAACTTAGAAACAGTTTAAAGTG 2220

QY 61 ATCTTAGAGTGTCCATCTGTCTGGAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 120
DB 180 ATCTTAGAGTGTCCATCTGTCTGGAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 239
QY 121 CACATATTTTGCAAAATTTTGCAAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 180
DB 240 CACATATTTTGCAAAATTTTGCAAGTGTGATCAAGGAACCTGTCTCCACAAAGTGTGAC 299
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DB 300 TGTCTTTTATGTAAGATGATATCAACAAAGGAGGCTTACAAAGAAAGTACGAGATTTAGT 359
QY 241 CAATCTGTGTGAAGAGCTATTGAAATCATTTTGTCTTTTCAAGTTGTGACACAGGTTTGAG 300
DB 360 CAATCTGTGTGAAGAGCTATTGAAATCATTTTGTCTTTTCAAGTTGTGACACAGGTTTGAG 419
QY 301 TATCCAAACAGCTATATTTTGCAAAAGGAGGCTTACAAAGAAAGTACGAGATTTAGT 360
DB 420 TATCCAAACAGCTATATTTTGCAAAAGGAGGCTTACAAAGAAAGTACGAGATTTAGT 479
QY 361 GAAGTTTCTATCATCCAAAGTATGGCTTACGAAACCGTGCACAAAGAGCTTCTACAGAT 420
DB 480 GAAGTTTCTATCATCCAAAGTATGGCTTACGAAACCGTGCACAAAGAGCTTCTACAGAT 539
QY 421 GAACCCGAAATCTCTTTCAGAGAACCAAGTCTCAGTGTCCAACTCTCTACCTTGA 480
DB 540 GAACCCGAAATCTCTTTCAGAGAACCAAGTCTCAGTGTCCAACTCTCTACCTTGA 599
QY 481 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTGTCTCAAT 540
DB 600 ACTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTGTCTCAAT 659
QY 541 GAATTTGGATCTGATCTTCTGAGAGATACCGTTAATGAAGGCACTTATTCAGTGTGGGA 600
DB 660 GAATTTGGATCTGATCTTCTGAGAGATACCGTTAATGAAGGCACTTATTCAGTGTGGGA 719
QY 601 GATCAAGATTTGTACAAATCAACCCCTCAAGGAACCGGATGAATCACTGTGATCT 660
DB 720 GATCAAGATTTGTACAAATCAACCCCTCAAGGAACCGGATGAATCACTGTGATCT 779
QY 661 GCAAAAAGGCTGTGTGAATTTCTGAGCGGATGAATCAATCTGAACTATCAATCA 720
DB 780 GCAAAAAGGCTGTGTGAATTTCTGAGCGGATGAATCAATCTGAACTATCAATCA 839
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QY 1081 TCAGAGAACTCTGAGATCTGAGAGATTTCTTGTGTAACACTTAAATAGCAGCATTCAG 1140
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QY 1201 GGGAGTCTGAATCAATCCAAAGTGTGATGATGATGATGATGATGATGATGATGATGATGAT 1260
DB 1320 GGGAGTCTGAATCAATCCAAAGTGTGATGATGATGATGATGATGATGATGATGATGAT 1379
QY 1261 GAATATTTCTGGTTCTTTCAGAGAAATAGACTTACTGCGCCAGTGTATCTCTATGAGGCTTTA 1320
DB 1380 GAATATTTCTGGTTCTTTCAGAGAAATAGACTTACTGCGCCAGTGTATCTCTATGAGGCTTTA 1439
QY 1321 ATATGTAAAGTGAAGAGTTCTCTCAATCAAGTGAAGTGAATTAATGAGAGCAAAATA 1380
DB 1440 ATATGTAAAGTGAAGAGTTCTCTCAATCAAGTGAAGTGAATTAATGAGAGCAAAATA 1499
QY 1381 TTTGGGAAACCTTATCGGAAGGAGGCAAGCTCCCAACTTAAAGCCATGTAACTGAAAAAT 1440
DB 1500 TTTGGGAAACCTTATCGGAAGGAGGCAAGCTCCCAACTTAAAGCCATGTAACTGAAAAAT 1559
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DB 1560 CTAAATATAGGAGCATTTGTTACTGAGCCACAGATTAATCAAGAGCGTCCCTCACAAT 1619
QY 1501 AAATTTAAAGCGTAAAGAGGAGCTTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAA 1560
DB 1620 AAATTTAAAGCGTAAAGAGGAGCTTACATCAGGCTTTCATCTGAGGATTTTATCAAGAAA 1679
QY 1561 GCAGATTTGGAGTTCAAAAGACTCTGAAATGATAAATCAAGGAACTTAAACCAAAAGGAG 1620
DB 1680 GCAGATTTGGAGTTCAAAAGACTCTGAAATGATAAATCAAGGAACTTAAACCAAAAGGAG 1739
QY 1621 CAGAAATGCTCAGTGTGATGATTAATTAATAGTGTGATGATGATGATGATGATGATGAT 1680
DB 1740 CAGAAATGCTCAGTGTGATGATTAATTAATAGTGTGATGATGATGATGATGATGAT 1799
QY 1681 TCTATTTCAAGATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTC 1740
DB 1800 TCTATTTCAAGATGAGAAAAATCTTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTC 1859
QY 1741 AAAAGCAAGTGAACCTTATGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 1800
DB 1860 AAAAGCAAGTGAACCTTATGAGGAGGATGATGATGATGATGATGATGATGATGATGAT 1919
QY 1801 CAAATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAAATCTTCTACAGGCAATTT 1860
DB 1920 CAAATTTCAAAAGCACTTAAAGAAATAGGCTGAGGAGGAAATCTTCTACAGGCAATTT 1979
QY 1861 CATGCGCTTGAATAGTACTCAGTGAATTTAAAGCCCACTTAAATGTTACTGAAATTCGAA 1920
DB 1980 CATGCGCTTGAATAGTACTCAGTGAATTTAAAGCCCACTTAAATGTTACTGAAATTCGAA 2039
QY 1921 ATTGATAGTTGTTCTAGCAGTGAAGTAAAGAAAGGATGATGATGATGATGATGATGAT 1980
DB 2040 ATTGATAGTTGTTCTAGCAGTGAAGTAAAGAAAGGATGATGATGATGATGATGATGAT 2099
QY 1981 AGGCAAGCAGAGAAACCTTCAAACTCATGGAAGGTAAGAAACCTTCAAACTGAGGCAAGAG 2040
DB 2100 AGGCAAGCAGAGAAACCTTCAAACTCATGGAAGGTAAGAAACCTTCAAACTGAGGCAAGAG 2159
QY 2041 AGTAAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTGTACTTTCCAGAGCTG 2100
DB 2160 AGTAAACAGCCAAATGAAACAGACAGTAAAGACATGACAGTGTACTTTCCAGAGCTG 2219
QY 2101 AAGTTAAACAAATGCACTGCTGTTCTTTTAAAGTGTTCAAATACCAAGTGAATCTTAAAGAA 2160
DB 2220 AAGTTAAACAAATGCACTGCTGTTCTTTTAAAGTGTTCAAATACCAAGTGAATCTTAAAGAA 2279
QY 2161 TTTGTCAATCTTAGGCTTCCAAAGAGAGAAAGAGAGAACTAGAAACAGTTAAAGTG 2220
DB 2280 TTTGTCAATCTTAGGCTTCCAAAGAGAGAAAGAGAGAACTAGAAACAGTTAAAGTG 2339
QY 2221 TCTTAATAGTGTGAAGAGCCCAAGATCTCTGTTAAAGTGAAGAGGCTTTTGCAAACT 2280

Db 2340 TCTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTTCAAAAC 2399
Qy 2281 GAAAGATCTGTAGAGAGTAGCAGATTTTCACTGCTACCTGGTACTGATTATGGCAGCTCAG 2340
Db 2400 GAAAGATCTGTAGAGAGTAGCAGATTTTCACTGCTACCTGGTACTGATTATGGCAGCTCAG 2459
Qy 2341 GAAAGATCTGTGTTACTGGAAGTAGCACTCTAGGGAAGGCAAAACAGAAACCAATATAA 2400
Db 2460 GAAAGATCTGTGTTACTGGAAGTAGCACTCTAGGGAAGGCAAAACAGAAACCAATATAA 2519
Qy 2401 TGTGTGAGTCACTGTGAGCAATTTGAACCCCAAGGAGTAAATCATGGTGTGTTCCAAA 2460
Db 2520 TGTGTGAGTCACTGTGAGCAATTTGAACCCCAAGGAGTAAATCATGGTGTGTTCCAAA 2579
Qy 2461 GATAATAGAAATGACACAGAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGT 2520
Db 2580 GATAATAGAAATGACACAGAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGT 2639
Qy 2521 CGGGAACAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCAGAAATACA 2580
Db 2640 CGGGAACAGCATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCAGAAATACA 2699
Qy 2581 TTCAAGGTTTCAAGGCGCAGTCATTGCTCTGTTTCAAAATCCAGGAAATGCAAGAGAG 2640
Db 2700 TTCAAGGTTTCAAGGCGCAGTCATTGCTCTGTTTCAAAATCCAGGAAATGCAAGAGAG 2759
Qy 2641 GAATGTGCAACATCTCTGCCACCTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACT 2700
Db 2760 GAATGTGCAACATCTCTGCCACCTCTGGGCTCTTAAAGAAACAAAGTCCAAAAGTCACT 2819
Qy 2701 TTGTAATGTGAACAAAGAGAGAAATCAAGAGAGAGTGAAGTCTAATATCAAGCTGTA 2760
Db 2820 TTGTAATGTGAACAAAGAGAGAAATCAAGAGAGAGTGAAGTCTAATATCAAGCTGTA 2879
Qy 2761 CAGACAGTTAATPATCACTGCGAGCTTCTCTGGTGTGTCAGAAAGATAAGCCAGTTGAT 2820
Db 2880 CAGACAGTTAATPATCACTGCGAGCTTCTCTGGTGTGTCAGAAAGATAAGCCAGTTGAT 2939
Qy 2821 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTCTCTATCATCTCAGTTCAGAGGC 2880
Db 2940 AATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTCTCTATCATCTCAGTTCAGAGGC 2999
Qy 2881 AACGAAACTGGACTCATTTACTCCAAATAAACATGAGCTTTTACAAAACCCATATCGTATA 2940
Db 3000 AACGAAACTGGACTCATTTACTCCAAATAAACATGAGCTTTTACAAAACCCATATCGTATA 3059
Qy 2941 CCACACATTTTCCCATCAAGTCATTTGTTTAAACTAAATGTAAGAAATCTCGTAGAG 3000
Db 3060 CCACACATTTTCCCATCAAGTCATTTGTTTAAACTAAATGTAAGAAATCTCGTAGAG 3119
Qy 3001 GAAACATTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAACATTTCCA 3060
Db 3120 GAAACATTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGGAAATGAGAAACATTTCCA 3179
Qy 3061 AGTACAGTGAACAAATGACCGTAAATACANTAGAGAAATGTTTTTAAAGGAGCCAGC 3120
Db 3180 AGTACAGTGAACAAATGACCGTAAATACANTAGAGAAATGTTTTTAAAGGAGCCAGC 3239
Qy 3121 TCAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATCAA 3180
Db 3240 TCAAGCAATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATCAA 3299
Qy 3181 ATAGGTTCCAGTGAATGAACAAATCAAGCAGAACTAGGTAGAAACAGAGGGGCCAAAATG 3240
Db 3300 ATAGGTTCCAGTGAATGAACAAATCAAGCAGAACTAGGTAGAAACAGAGGGGCCAAAATG 3359
Qy 3241 AATGCTATGCTTAGATTAGGGGTTTGCACCTGAGGCTATATAACAAAGTCTTCTGGA 3300
Db 3360 AATGCTATGCTTAGATTAGGGGTTTGCACCTGAGGCTATATAACAAAGTCTTCTGGA 3419
Qy 3301 AGTAATTTGAAGCATCTCTGAAATAAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTT 3360
Db 3420 AGTAATTTGAAGCATCTCTGAAATAAAGCAAGAAATATGAAGAGTAGTTTCAGACTGTT 3479

Qy 3361 AATACAGATTTCTCTCCATATCTGATTTTCAGATAAATTAGAACAGCCTATGGGAAGTAGT 3420
Db 3480 AATACAGATTTCTCTCCATATCTGATTTTCAGATAAATTAGAACAGCCTATGGGAAGTAGT 3539
Qy 3421 CATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATATAAG 3480
Db 3540 CATGCATCTCAGGTTGTTCTGAGACACCTGATGACCTGTTAGATGATGTTGAAATATAAG 3599
Qy 3481 GAAGATATCTAGTTTCTGANAATGACATTAAGGAAAGTTCTGCTGTTTTTACAAAAGC 3540
Db 3600 GAAGATATCTAGTTTCTGANAATGACATTAAGGAAAGTTCTGCTGTTTTTACAAAAGC 3659
Qy 3541 GTCCAGAGAGAGAGCTTACGAGAGTCTTAGGCCCTTACCCTATACATTTTGGCTCAG 3600
Db 3660 GTCCAGAGAGAGAGCTTACGAGAGTCTTAGGCCCTTACCCTATACATTTTGGCTCAG 3719
Qy 3601 GGTTCACGAAGAGGGCCCAAGAAATTAGAGTCTCTAGAGAGAGAACTTATCTAGTGAGGAT 3660
Db 3720 GGTTCACGAAGAGGGCCCAAGAAATTAGAGTCTCTAGAGAGAGAACTTATCTAGTGAGGAT 3779
Qy 3661 GAAGAGCTTCCCTGCTTCCAAACACTTGTATTGTTGTTAAAGTAAACATATACCTTCTCAG 3720
Db 3780 GAAGAGCTTCCCTGCTTCCAAACACTTGTATTGTTGTTAAAGTAAACATATACCTTCTCAG 3839
Qy 3721 TCTACTAGGCATACACCGTTGCTACCGAGTCTCTCTAAGAAACACAGAGAGAAATTTA 3780
Db 3840 TCTACTAGGCATACACCGTTGCTACCGAGTCTCTCTAAGAAACACAGAGAGAAATTTA 3899
Qy 3781 TTATCATTTGAAGATAGCTTAAATGATCTCAGTAAACAGGTAATATTGGCAAGGCAATCT 3840
Db 3900 TTATCATTTGAAGATAGCTTAAATGATCTCAGTAAACAGGTAATATTGGCAAGGCAATCT 3959
Qy 3841 CAGGAACATCACCTTATAGTGAGGAAACAAATGTTCTGCTAGCTGTTTCTTCCACAGTGC 3900
Db 3960 CAGGAACATCACCTTATAGTGAGGAAACAAATGTTCTGCTAGCTGTTTCTTCCACAGTGC 4019
Qy 3901 AGTGAATTTGAACACTTGAATGCAAAATCAAAACCCAGGATCTTTCTTGAATGTTCT 3960
Db 4020 AGTGAATTTGAACACTTGAATGCAAAATCAAAACCCAGGATCTTTCTTGAATGTTCT 4079
Qy 3961 TCCAAAACAAATGAGGCAATGCTGAAAGCCAGGAGTGGTCTGAGTGACAGGAAATG 4020
Db 4080 TCCAAAACAAATGAGGCAATGCTGAAAGCCAGGAGTGGTCTGAGTGACAGGAAATG 4139
Qy 4021 GTTTCAGATCATGAAGAGAGGAAACGGGCTTGGAAAGAAATTAATCAAGAGAGCAAAAGC 4080
Db 4140 GTTTCAGATCATGAAGAGAGGAAACGGGCTTGGAAAGAAATTAATCAAGAGAGCAAAAGC 4199
Qy 4081 ATGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACACAGCGTCTCTGAA 4140
Db 4200 ATGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACACAGCGTCTCTGAA 4259
Qy 4141 GACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG 4200
Db 4260 GACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG 4319
Qy 4201 CAACATAACCTGATAAAGCTTCCAGCAGGAAATGGCTGAACTAGAGAGTGTGTTAGAAACAG 4260
Db 4320 CAACATAACCTGATAAAGCTTCCAGCAGGAAATGGCTGAACTAGAGAGTGTGTTAGAAACAG 4379
Qy 4261 CATGGGAGCAGCGCTTCTACAGCTACCTTCCATCATATAAGTGAATCTTGTGCGCTTGA 4320
Db 4380 CATGGGAGCAGCGCTTCTACAGCTACCTTCCATCATATAAGTGAATCTTGTGCGCTTGA 4439
Qy 4321 GACTGCGAAATCCAGAAACAAAGCACATCAAGAAAGCAGTATTAATCTCAGAAAGT 4380
Db 4440 GACTGCGAAATCCAGAAACAAAGCACATCAAGAAAGCAGTATTAATCTCAGAAAGT 4499
Qy 4381 AGTGAATACCTTAAAGCCAGAAATCCAGAGGCTTCTGCTGACAGGTTTGGAGTCTCT 4440
Db 4500 AGTGAATACCTTAAAGCCAGAAATCCAGAGGCTTCTGCTGACAGGTTTGGAGTCTCT 4559

Db	2400	GAAGAATCTGTGAGAGTAGCAGTATTTCATCTGGTACCTGGTACTGATTAATGCGCACTCAG	2455
Qy	2341	GAAGAATATCTCGTTTACTTGGAAAGTTAGCACCTCTAGGGAAGGCAAAAACAGAACCAAATAAA	2400
Db	2460	GAAGATATCTCGTTACTGGAGTTAGCACTCTAGGGAGGCAAAACAGACACCAATATA	2519
Qy	2401	TGTGTGAGTCAGTGTGCGAGCATTTTGAAAAACCCCAAGGGACTAAATTCATGTGTTTCCAAA	2460
Db	2520	TGTGTGAGTCAGTGTGCGAGCATTTTGAAAAACCCCAAGGGACTAAATTCATGTGTTTCCAAA	2579
Qy	2461	GATAATAGAAATGACACAGAAAGCTTTAAGTATTCATTTGGGACATCAAGTTTAAACCAAGT	2520
Db	2580	GATPATAGAAATGACACAGAAAGCTTTAAGTATTCATTTGGGACATCAAGTTTAAACCAAGT	2639
Qy	2521	CGGGAAACAAGCATAGAAATGGAAGAAAGTGAACTTGATGCTCAGTATTTGCGAGAAATACA	2580
Db	2640	CGGGAAACAAGCATAGAAATGGAAGAAAGTGAACTTGATGCTCAGTATTTGCGAGAAATACA	2699
Qy	2581	TTCAAGGTTTCAAGGCGCCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAATGCGAAGAG	2640
Db	2700	TTCAAGGTTTCAAGGCGCCAGTCAATTTGCTCTGTTTTCAAAATCCAGGAATGCGAAGAG	2759
Qy	2641	GAATGTGCAACATTTCTCTGCCCACTCTGGGTCCTTTAAAGAAACAAAAGTCCAAAAGTCAC	2700
Db	2760	GAATGTGCAACATTTCTCTGCCCACTCTGGGTCCTTTAAAGAAACAAAAGTCCAAAAGTCAC	2819
Qy	2701	TTTGAATGTGCAACAAAGGAAGAAATCAAGGAAGGATCAGTCTAATATCAAGCCGTGTA	2760
Db	2820	TTTGAATGTGCAACAAAGGAAGAAATCAAGGAAGGATCAGTCTAATATCAAGCCGTGTA	2879
Qy	2761	CAGACAGTAAATATCACTGCGAGGCTTTCCCTGTGTGTTGGTCAGAAAGATAGCCAGTTGAT	2820
Db	2880	CAGACAGTAAATATCACTGCGAGGCTTTCCCTGTGTGTTGGTCAGAAAGATAGCCAGTTGAT	2939
Qy	2821	AATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCATATCATCTCAGTTTCAGAGGC	2880
Db	2940	AATGCCAAATGTAGTATCAAAAGGAGGCTCTAGGTTTTGTCATATCATCTCAGTTTCAGAGGC	2999
Qy	2881	AACGMAACTGSACTCATTTACTCCAAATAAACATGAGACTTTTACAAAACCCATATCGTATA	2940
Db	3000	AACGMAACTGSACTCATTTACTCCAAATAAACATGAGACTTTTACAAAACCCATATCGTATA	3059
Qy	2941	CCACCCTTTTCCCATCAAGTCAATTTGTTTAAACCTAAATGTGAAGAAAAATCTGCTAGAG	3000
Db	3060	CCACCCTTTTCCCATCAAGTCAATTTGTTTAAACCTAAATGTGAAGAAAAATCTGCTAGAG	3119
Qy	3001	GAAGCTTTGAGGAACATTCATCTCACCCTGGAAGAGAAATGGGAATGAGAACATTTCCA	3060
Db	3120	GAAGCTTTGAGGAACATTCATCTCACCCTGGAAGAGAAATGGGAATGAGAACATTTCCA	3179
Qy	3061	AGTACAGTGAGCACAATTTAGCCCGTAATAACAATTAGAGAAAAATGTTTTTAAAGAGGCCAGC	3120
Db	3180	AGTACAGTGAGCACAATTTAGCCCGTAATAACAATTAGAGAAAAATGTTTTTAAAGAGGCCAGC	3239
Qy	3121	TCAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGA	3180
Db	3240	TCAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGCTCCAGTATTAATGA	3299
Qy	3181	ATAGGTTCCAGTGATGAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGCGCCAAAATTG	3240
Db	3300	ATAGGTTCCAGTGATGAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGCGCCAAAATTG	3359
Qy	3241	AATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGTCTATAAACAAAGTCTTCCTGGGA	3300
Db	3360	AATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGTCTATAAACAAAGTCTTCCTGGGA	3419
Qy	3301	AGTAATTTGTAAGCATCTCTGAATATAAAAAAGCAAGATATGAAGAAGTAGTTTCAGACTGTT	3360
Db	3420	AGTAATTTGTAAGCATCTCTGAATATAAAAAAGCAAGATATGAAGAAGTAGTTTCAGACTGTT	3479
Qy	3361	AATAAGATTTCTCTCCATATCTCATTTTCAGATTAACCTTGAAGCAAGCCTTATGGGAAGTAGT	3420
Db	3480	AATAAGATTTCTCTCCATATCTCATTTTCAGATTAACCTTGAAGCAAGCCTTATGGGAAGTAGT	3539

Qy	3421	CATGCATCTCAGGTTTGTCTCAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG	3488
Db	3540	CATGCATCTCAGGTTTGTCTCAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG	3599
Qy	3481	GAAGATACTAGTTTGTCTGAAATAGCATTAAGAGAAAGTTCTGCTGTTTTTATGACAAAGC	3540
Db	3600	GAAGATACTAGTTTGTCTGAAATAGCATTAAGAGAAAGTTCTGCTGTTTTTATGACAAAGC	3659
Qy	3541	GTCAGAGAGGAGAGCTTTAGCAGGAGTCTCTAGCCCTTTTACCCATACACATTGTGGCTCAG	3600
Db	3660	GTCAGAGAGGAGAGCTTTAGCAGGAGTCTCTAGCCCTTTTACCCATACACATTGTGGCTCAG	3719
Qy	3601	GGTTTACCAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTCAGGAT	3660
Db	3720	GGTTTACCAGAGGGGCCAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTCAGGAT	3779
Qy	3661	GAAGAGCTTCCCTGCTTCCAAACACTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAG	3720
Db	3780	GAAGAGCTTCCCTGCTTCCAAACACTTGTTATTTGGTAAAGTAAACAAATATACCTTCTCAG	3839
Qy	3721	TCTACTAGGCATAGCACCGTCTGTACCGGAGTGTCTGTTAAGAACACAGAGGAGAAATTTA	3780
Db	3840	TCTACTAGGCATAGCACCGTCTGTACCGGAGTGTCTGTTAAGAACACAGAGGAGAAATTTA	3899
Qy	3781	TTATCATTTGAGAAATAGCTTTAATGTACTGCTACCGAGTAAATATGCGCAAGGCAATCT	3840
Db	3900	TTATCATTTGAGAAATAGCTTTAATGTACTGCTACCGAGTAAATATGCGCAAGGCAATCT	3959
Qy	3841	CAGCAACATCACCTTAGTCAGGAGAAACAAATGTTCTGCTAGCTTGTTTTCTTCACAGTGC	3900
Db	3960	CAGCAACATCACCTTAGTCAGGAGAAACAAATGTTCTGCTAGCTTGTTTTCTTCACAGTGC	4019
Qy	3901	AGTGAATTTGAGAGACTTGACTGCAANATCAAAACCCAGGATCCTTTCTTGATGGTCTCT	3960
Db	4020	AGTGAATTTGAGAGACTTGACTGCAANATCAAAACCCAGGATCCTTTCTTGATGGTCTCT	4079
Qy	3961	TCCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAAGGAATTC	4020
Db	4080	TCCAAACAAATGAGGCATCAGTCTGAAAGCCAGGGAGTTGGTCTGAGTGACAAAGGAATTC	4139
Qy	4021	GTTTTCAGATGATGAAGAGAGGAGACGGCTTGGAGAGAAATAATCAAGAGAGGCAAAAGC	4080
Db	4140	GTTTTCAGATGATGAAGAGAGGAGACGGCTTGGAGAGAAATAATCAAGAGAGGCAAAAGC	4199
Qy	4081	ATGCAATTCAAACTTAGTGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAGCGTCTCTGAA	4140
Db	4200	ATGCAATTCAAACTTAGTGTGAAGCAGCATCTGGGTGTGAGAGTGAAACAAGCGTCTCTGAA	4259
Qy	4141	GACTGCTCAGGGCTATCCTCTCAGATGTGACATTTTAAACCATCTCAGCAGAGGAGATACCATG	4200
Db	4260	GACTGCTCAGGGCTATCCTCTCAGATGTGACATTTTAAACCATCTCAGCAGAGGAGATACCATG	4319
Qy	4201	CAACATAACTGATAAAGCTCCACAGAGGAAATGGCTGAACTAGAGTGAAACAGAGCAG	4260
Db	4320	CAACATAACTGATAAAGCTCCACAGAGGAAATGGCTGAACTAGAGTGAAACAGAGCAG	4379
Qy	4261	CATGGGAGCCAGGCTTCTAAGCTACCTTCCATCATAGTGACATTTGTCGCCCTTGAG	4320
Db	4380	CATGGGAGCCAGGCTTCTAAGCTACCTTCCATCATAGTGACATTTGTCGCCCTTGAG	4439
Qy	4321	GACTCGCAAAATCCAGAACAAAGCAGATCAGAAAAAGCAGATTTAACTTCCAGAAAAAGT	4380
Db	4440	GACTCGCAAAATCCAGAACAAAGCAGATCAGAAAAAGCAGATTTAACTTCCAGAAAAAGT	4499
Qy	4381	AGTCAATACCTTATAGCCAGAAATCCAGAGGCTTCTTCTGCTCAACAAGTTTGAAGTGTCT	4440
Db	4500	AGTCAATACCTTATAGCCAGAAATCCAGAGGCTTCTTCTGCTCAACAAGTTTGAAGTGTCT	4559
Qy	4441	GCAGATAGTTCTACCAAGTAAAAATAAGAACCCAGGAGTGAAAGTGATCCCTCTCTAAA	4500
Db	4560	GCAGATAGTTCTACCAAGTAAAAATAAGAACCCAGGAGTGAAAGTGATCCCTCTCTAAA	4619

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 4861 GATAGTCTGGGTATATGCAATGAAAGTGTGACGAGGAGGAGGAGGAGGAGGAGGAG 4920
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 5581 AGCCACTAC 5589

Db 5700 AGCCACTAC 5708
 RESULT 6
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 ; Sequence 1, Application US/08825487A
 ; Patent No. 6048689
 ; GENERAL INFORMATION:
 ; APPLICANT: Murphy, Patricia D.
 ; APPLICANT: White, Marga B.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC
 ; NUMBER OF SEQUENCES: 110
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howrey & Simon
 ; STREET: 1299 Pennsylvania Avenue., N.W.
 ; CITY: Washington,
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
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 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5711 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORIGINAL SOURCE:
 ; ORGANISM: Homo sapiens
 ; STRAIN: BRC41
 ; POSITION IN GENOME:
 ; CHROMOSOME/SEGMENT: 17
 ; MAP POSITION: 17q21
 ; US-08-825-487A-1
 Query Match 100.0%; Score 5587.4; DB 3; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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 Db 540 GAA CCGGAAAATCTCTCTCTGAGGAAACCAAGCTCTCAGTGTCCAACTCTCTAACTTTGA 599
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 Qy 601 GATCAGAAATGTTTAAATCAACCTCTCAAGGAAACCGAGGATGAAATCAGTTTGGATTCT 660
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 Qy 721 CCAAGTAAATGATTTGAAACCAACCTCTCAAGGAAACCGAGGATGAAATCAGTTTGG 780
 Db 840 CCAAGTAAATGATTTGAAACCAACCTCTCAAGGAAACCGAGGATGAAATCAGTTTGG 899
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 Db 900 TATCAGGATGTTCTGTTTCAAACTCTGAGGATGTTTCAAGGATGTTTCAAGGATGTT 959
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 Qy 901 AAGCTGAATCTGTATTAAGAAACAGCAGCTTGTCTTACAGGAGGCAACATACAGAA 960
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 Qy 1021 GATCTGAATGTTGATCCCTGTGTGAGAGAAAGATGGAATGGAATGGAATGGAATGGA 1080
 Db 1140 GATCTGAATGTTGATCCCTGTGTGAGAGAAAGATGGAATGGAATGGAATGGAATGGA 1199
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 Db 1200 TCAGAGAACTCTGAGATCTGAGAGTTTCTTTGATTAACACTTAAATAGCAGCACTTCA 1259
 Qy 1141 AAAGTTAATGATGGTTTTCAGAGAGTGTAACTGTTGATGTTCTGATGATCTCAGAT 1200
 Db 1260 AAAGTTAATGATGGTTTTCAGAGAGTGTAACTGTTGATGTTCTGATGATCTCAGAT 1319
 Qy 1201 GGGAGTCTGAATCAAAATGCAAGTACTGATGTTGATGTTCTGATGATCTCAGAT 1260
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 Qy 1261 GAATATTCTGTTTCTTCAAGAGAAATAGACTTACTGCGCAGTGTATCTCTATGAGGCTTTA 1320
 Db 1380 GAATATTCTGTTTCTTCAAGAGAAATAGACTTACTGCGCAGTGTATCTCTATGAGGCTTTA 1439

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 Db 1740 CAGATGTTCAAGTGTATGATTAATTAATAGTGTCTGATGAGATAAACAAGAGTGTAT 1799
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Db 3660 GTCCAGAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTTCCACCATACACATTTGGCTCAG 3719
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QY 4021 GTTTCAGATGATGAGAAAGAGGACGGGCTTTGGAGAAATAATCAAGAGAGCAAGC 4080
Db 4140 GTTTCAGATGATGAGAAAGAGGACGGGCTTTGGAGAAATAATCAAGAGAGCAAGC 4199
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Db 4200 ATGGATTTCAAACTTAGGTGACGAGCATCTGGGTTGTGAGAGTGAACAGAGCTCTCTGAA 4259
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Db 4320 CAACATAAAGCTGATAAAGCTCCAGCAGGAAATGGGCTGAAGTGAAGCTGTGTAGAACAG 4379
QY 4261 CATGGAGCCAGCTTCTTAACAGTACCTTCCATCATTAAGTGAATTTCTCCCTCTGAG 4320
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[illegible]

RESULT 7

US-09-074-476-1

Sequence 1, Application US/09074476
Patent No. 6130322
GENERAL INFORMATION:
APPLICANT: Murphy, Patricia D.
APPLICANT: Allen, Antonette C.
APPLICANT: Alvares, Christopher P.
APPLICANT: Critz, Shendi S.
APPLICANT: Olson, Sheri J.
APPLICANT: Thurber, Denise
APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
TITLE OF INVENTION: BRCAL Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSES: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL (gm11)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-09-074-476-1

	Query Match	100.0.0%;	Score 5587.4;	DB 3;	Length 5711;
	Best Local Similarity	100.0.0%;	Pred. No. 0;		
	Matches 5588;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
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Qy	61	ATCTTAGAGTGTCCCATCTCTCTGGAGTGTGATCAAGGAACTGTCTCTCCACAAAGTGTGAC	120		
Db	180	ATCTTAGAGTGTCCCATCTCTCTGGAGTGTGATCAAGGAACTGTCTCTCCACAAAGTGTGAC	239		
Qy	121	CACATATTTTGGCAAAATTTTGCATGCTCAAACTTCTCAACCAAGAAAGGGCCCTTCACAG	180		
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Qy	181	TGTCCTTTATGTGAAGATGATATAACCAAAAGGAGGCCTTACAAGAAAGTACGAGATTTTAGT	240		
Db	300	TGTCCCTTTATGTGAAGATGATATAACCAAAAGGAGGCCTTACAAGAAAGTACGAGATTTTAGT	359		

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QY 4921 GCTTCAACAGAGAGGCTCAACAAAGAAATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCT 4980
Db 5040 GCTTCAACAGAGAGGCTCAACAAAGAAATGTCATGTTGCTGCTGCTGCTGCTGCTGCTGCT 5099
QY 4981 GAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
Db 5100 GAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5159
QY 5041 ACTGAAGAGACTACTCATGTTGTTATGAACAGATGCTGAGTGTGTTGTTGTTGTTGTTGTT 5100
Db 5160 ACTGAAGAGACTACTCATGTTGTTATGAACAGATGCTGAGTGTGTTGTTGTTGTTGTTGTT 5219
QY 5101 CTGAATATTTCTAGGAATTCGCGAGGAGAAATGGGTAGTGTAGTATTTCTGGGTGACC 5160
Db 5220 CTGAATATTTCTAGGAATTCGCGAGGAGAAATGGGTAGTGTAGTATTTCTGGGTGACC 5279
QY 5161 CAGTCTATTAAAGAGAAATGCTGATGAGATGATGATGATGATGATGATGATGATGATGATG 5220
Db 5280 CAGTCTATTAAAGAGAAATGCTGATGAGATGATGATGATGATGATGATGATGATGATG 5339
QY 5221 GTCAATGAAGAAACCAACCAAGGCTCCAAAGCGAGCAAGAGAAATCCAGGACAGAAAGATC 5280
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Db 5700 AGCCACTAC 5708

RESULT 8

US-10-022-819-1

; Sequence 1, Application US/10022819

; Patent No. 5686163
; GENERAL INFORMATION:
; APPLICANT: ALLEN, Antonette C. P.
; OLSEN, Sheri J.
; LAWRENCE, Tammy
; ANGELLY, Tracy S.
; PABIN, Mark B.
; TITLE OF INVENTION: CODING SEQUENCE HAPLOTYPE OF THE HUMAN
; BRCAL GENE
; NUMBER OF SEQUENCES: 67
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Morgan Lewis & Bockius LLP
; STREET: 1111 Pennsylvania Avenue
; CITY: Washington DC
; STATE: District of Columbia
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/022,819
; FILING DATE: 22-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/074,452
; FILING DATE: 1998-05-06
; ATTORNEY/AGENT INFORMATION:
; NAME: <Unknown>
; REGISTRATION NUMBER: <Unknown>
; REFERENCE/DOCKET NUMBER: 044921-5049-01-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-739-3000
; TELEFAX: 202-739-3001
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; STRAIN: BRCAL
; HAPLOTYPE: OM14
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17
; MAP POSITION: 17q21
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-022-819-1

Query Match 99.9%; Score 5585.8; DB-4; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5587; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 ATGGATTATCTGCTCTTCGCGTTGGAAGATACAAATGTCTCAATTAATGCTATGAGAA 60
Db 120 ATGGATTATCTGCTCTTCGCGTTGGAAGATACAAATGTCTCAATTAATGCTATGAGAA 179
QY 61 ATCTTAGAGTGCCCATCTGCTGAGTGTGATCAAGAACCTGTCTCCACAAAGTGTGAC 120
Db 180 ATCTTAGAGTGCCCATCTGCTGAGTGTGATCAAGAACCTGTCTCCACAAAGTGTGAC 239
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Db 360 CAACCTTGTGAAGAGCTATTGAAATCAITTTGTGCTTTTTCAGCTTGTGACACAGGTTTGGAG 419
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Qy 361 GAAGTTTCTATCTCAAAAGTATGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 420
Db 480 GAAGTTTCTATCTCAAAAGTATGGCTACAGAAACCGTCCCAAAAGACTTCTACAGAGT 539
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Db 540 GAACCCGAAATCTTCTTCTGAGGAAACCAAGCAGCGGATACAACTCAAAAGAGCTTCTACAGAGT 599
Qy 481 ACTGTGAGAACTCTGAGGAAACCAAGCAGCGGATACAACTCAAAAGAGCTTCTACAGAGT 540
Db 600 ACTGTGAGAACTCTGAGGAAACCAAGCAGCGGATACAACTCAAAAGAGCTTCTACAGAGT 659
Qy 541 GAATTCGGATCTGATCTTCTGAGGAAACCAAGCAGCGGATACAACTCAAAAGAGCTTCTACAGAGT 600
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Qy 601 GATCAAGAAATTTGTATCAAAATCAACCTCAAGGAAACCAAGGAGTAAATCAGTTTGGATCT 660
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Qy 661 GCAAAAAGGCTCTGTTGAAATTTCTGAGACGATGTAACAAATCTGAAACATCATCAA 720
Db 780 GCAAAAAGGCTCTGTTGAAATTTCTGAGACGATGTAACAAATCTGAAACATCATCAA 839
Qy 721 CCCAGTAATAAGATTTGAAACCACTGAGAGGCTGAGAGGCAATCCAGAAAG 780
Db 840 CCCAGTAATAAGATTTGAAACCACTGAGAGGCTGAGAGGCAATCCAGAAAG 899
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Db 900 TATCAGGCTAGTTCTGTTTCAAACTTGCATGTGAGGCAATGTCGCAAAATCTCATGCC 959
Qy 841 AGCTCATATACAGATGAGACAGCAGTTTATCTCACTAAAGACAGAAATGATAGAA 900
Db 960 AGCTCATATACAGATGAGACAGCAGTTTATCTCACTAAAGACAGAAATGATAGAA 1019
Qy 901 AAGGCTGAATTTCTGTAATAAAGCAACAGCCTGCTTAGCAAGGAGCCACATACAGA 960
Db 1020 AAGGCTGAATTTCTGTAATAAAGCAACAGCCTGCTTAGCAAGGAGCCACATACAGA 1079
Qy 961 TGGGCTGGAAGTAAGGAAACATGTATGATAGGCGGACTCCAGCAAGAAAGGTA 1020
Db 1080 TGGGCTGGAAGTAAGGAAACATGTATGATAGGCGGACTCCAGCAAGAAAGGTA 1139
Qy 1021 GATCTGAATGCTGATCCCTGCTGAGAGAAAGAAATGGAATGAATAGCAGCAATCCAG 1080
Db 1140 GATCTGAATGCTGATCCCTGCTGAGAGAAAGAAATGGAATGAATAGCAGCAATCCAG 1199
Qy 1081 TCAGAGAAATCTAGAGATATCTGAAGATGTTCTTGGATAACCTAAATAGCAGCAATCCAG 1140
Db 1200 TCAGAGAAATCTAGAGATATCTGAAGATGTTCTTGGATAACCTAAATAGCAGCAATCCAG 1259
Qy 1141 AAAGTTAATGAGGTTTTCAGAGATGATGAATCTGTTAGGTTCTGATGATCTCATGAT 1200
Db 1260 AAAGTTAATGAGGTTTTCAGAGATGATGAATCTGTTAGGTTCTGATGATCTCATGAT 1319
Qy 1201 GGGGAGTCTGAATCAAAATCCAAAGTAGCTGATGATGATGAGGTTCTAAATGAGGTAGAT 1260
Db 1320 GGGGAGTCTGAATCAAAATCCAAAGTAGCTGATGATGATGAGGTTCTAAATGAGGTAGAT 1379
Qy 1261 GAAATTTCTGTTTCTCAGAGAAATATAGACTTCTGAGGCAAGTATCTCATGAGGCTTTA 1320

Db 1380 GAATATTTCTGGTTCTTTCAGAGAAATATAGACTTACTGGCCAGTGATCCTCATGAGGCTTTA 1439
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Db 1440 ATATGTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGTAATATTCAGAGCAAAATA 1499
Qy 1381 TTTGGGAAACCTATTCGGAGAAAGGAGCCCTCCCACTTAAGCCATGTAACTGAAAT 1440
Db 1500 TTTGGGAAACCTATTCGGAGAAAGGAGCCCTCCCACTTAAGCCATGTAACTGAAAT 1559
Qy 1441 CTAATTTATAGGAGCATTTGTTACTGAGCCACAGATAATAACAAGAGCTCCCTCACAAT 1500
Db 1560 CTAATTTATAGGAGCATTTGTTACTGAGCCACAGATAATAACAAGAGCTCCCTCACAAT 1619
Qy 1501 AAATTTAAGCGTAAAGAGGAGCTTACATCAGGCCCTTCTCTGAGGATTTTATCAAGAA 1560
Db 1620 AAATTTAAGCGTAAAGAGGAGCTTACATCAGGCCCTTCTCTGAGGATTTTATCAAGAA 1679
Qy 1561 GCAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGGAACCTAACCAACGGAG 1620
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Db 1740 CAGAAATGCTCAAGTCAATTAATTTCTAATAGTGTCTATGAGAAATAAAACAAAGGTGAT 1799
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Db 1800 TCTATTTCAAGATGAGAAATCTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCTTAAACCT 1859
Qy 1741 AAACGAAAGCTGAACTTAAAGCAGAGTATTAAGCAATATGGAATCGAATTAATATATC 1800
Db 1860 AAACGAAAGCTGAACTTAAAGCAGAGTATTAAGCAATATGGAATCGAATTAATATATC 1919
Qy 1801 CAAATTTCAAAGCCTTAAAGAAATAGGCTGAGGAGAAAGTCTTCTACAGGCAATAT 1860
Db 1920 CAAATTTCAAAGCCTTAAAGAAATAGGCTGAGGAGAAAGTCTTCTACAGGCAATAT 1979
Qy 1861 CATGGCTTTGAATCAGTAGTAATCTTAAGCCACCTAATTTGTACTGAAATTCGAA 1920
Db 1980 CATGGCTTTGAATCAGTAGTAATCTTAAGCCACCTAATTTGTACTGAAATTCGAA 2039
Qy 1921 ATTGATGTTCTTCTAGCAGTGAAGATAAAGAAAGTAAACCAATGCCAGTCT 1980
Db 2040 ATTGATGTTCTTCTAGCAGTGAAGATAAAGAAAGTAAACCAATGCCAGTCT 2099
Qy 1981 AGGCACAGCAGAACTTACACTCATGAGGTAAGAACTGCAACTGGAGCCAGAG 2040
Db 2100 AGGCACAGCAGAACTTACACTCATGAGGTAAGAACTGCAACTGGAGCCAGAG 2159
Qy 2041 AGTAACCAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGAATCTTTCCAGAGCTG 2100
Db 2160 AGTAACCAAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGAATCTTTCCAGAGCTG 2219
Qy 2101 AAGTTTAACTGATGACCTGCTGTTCTTCTTAAAGTGTCAATACCACTGAGACTTAAAGAA 2160
Db 2220 AAGTTTAACTGATGACCTGCTGTTCTTCTTAAAGTGTCAATACCACTGAGACTTAAAGAA 2279
Qy 2161 TTTGTCATCTCTAGCCTTCCAGAGAAAGAAAGAGAGAACTAGAAACAGTTTAAAGTG 2220
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Qy 2221 TCTAATTAATGCTGAGAGCCCAAGATCTCATGTTAAGTGTGAGAAAGGTTTTCAGAACT 2280
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2521 CGGGAACCAAGCAATAGAAATGGAAGAGTGAACCTTGATGCTCAGTATTTGCGAGATACA 2580
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3001 GAAAACTTTGAGGACATCAATGTCACCTGAAAGGAATGGAATGGAATGGAATGGAATGGAAT 3060
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3181 ATAGGTTCCAGTATGAAACATCAAGCAGAACTAGTAGAAACAGAGGCCCCAAATTTG 3240
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3241 AATGCTATGCTTAGATTTAGGGGTTTTCACCTGAGGCTATGAAACAAAGTCTTCTGGA 3300
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Db CATGCATCTCAGGTTTGTCTGAGACCTGATGACCTGTTAGATGATGATGATGATGATGATGAT 3599

3481 GAAGATACCTAGTCTGCTGAAATGACATTAAGGAAAGTTCTGCTGTTTCTGCTGCTGCTGCTGCT 3540
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3541 GTCCAGAGAGGAGAGCTTAGCAGGAGTCTAGCCCTTTCAACCATACACATTTGGCTCAG 3600
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Db TCCAAACAAATGAGGAGTCTGCTGAAAGCCAGGAGTGTGCTGAGTGAAGAGGATTTG 4139
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4201 CAAATTAACCTGATTAAGCTCCAGAGGAAATGCTGAACTAGAGCTGTGTTAGAACAG 4260
Db CAAATTAACCTGATTAAGCTCCAGAGGAAATGCTGAACTAGAGCTGTGTTAGAACAG 4379
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4381 AGTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGAGCAAGTTTGGAGTGTCT 4440
Db AGTGAATACCTTATTAAGCCAGAAATCCAGAGGCTTTCTGCTGAGCAAGTTTGGAGTGTCT 4559
4441 GCAGATGTTCTACAGTAAATAAAGAAACAGAGGAGGAGGATCAATCCCTTCTTAA 4500
Db GCAGATGTTCTACAGTAAATAAAGAAACAGAGGAGGAGGATCAATCCCTTCTTAA 4619
4501 TGCCCATCATTTAGATGATGAGTGTGATGACAGAGTGTGCTGCTGAGGATTTTCAAGATAGA 4560
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4681 ACCCTTACCTGGAATCTGGAATCAGCTCTCTCTGATGACCTTGAATCTGATCTCTCT 4740
4800 ACCCTTACCTGGAATCTGGAATCAGCTCTCTCTGATGACCTTGAATCTGATCTCTCT 4859
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4920 AAGATTTCCCAATTTGAAGTTGAGATCTGCCAGGGTCCAGCTCTGCTCTCATCTACT 4979
4861 GATATCTCTGGGTATATGTAATGGAAGAAAGTGTGAGCAGGGAGGAGCCAGAAATGACA 4920
4980 GATATCTCTGGGTATATGTAATGGAAGAAAGTGTGAGCAGGGAGGAGCCAGAAATGACA 5039
4921 GCTTCAACAGAAAGGTCAACAAAGATGTCCATGTTGTTGCTGCTGCTGCTGCTGCTGCT 4980
5040 GCTTCAACAGAAAGGTCAACAAAGATGTCCATGTTGTTGCTGCTGCTGCTGCTGCTGCT 5099
4981 GAATTTATGCTCTGTAAGTTGTCAGAAATGTCAGAAATGTCAGAAATGTCAGAAATG 5040
5100 GAATTTATGCTCTGTAAGTTGTCAGAAATGTCAGAAATGTCAGAAATGTCAGAAATG 5159
5041 ACTGAGAGAGTACTCATGTTGTTATGAAACAGATGCTGAGTTGTTGTTGTTGTTGTTG 5100
5160 ACTGAGAGAGTACTCATGTTGTTATGAAACAGATGCTGAGTTGTTGTTGTTGTTGTTG 5219
5101 CTGAATATTTTCTAGCAATTTGGGAGGAAATGCTGATGATGATGATGATGATGATGATG 5160
5220 CTGAATATTTTCTAGCAATTTGGGAGGAAATGCTGATGATGATGATGATGATGATGATG 5279
5161 CAGTCTATTAAAGAAAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATG 5220
5280 CAGTCTATTAAAGAAAGAAATGCTGATGATGATGATGATGATGATGATGATGATGATG 5339
5221 GTCAATGGAAGAAACCAAGGTCACAAAGCGGAGGAGATCCAGGAGCAGAAAGATC 5280
5340 GTCAATGGAAGAAACCAAGGTCACAAAGCGGAGGAGATCCAGGAGCAGAAAGATC 5399
5281 TTCAGGGGCTAGAAATCTGTTGCTATGGGCTTCCACCAATGCTCCACAGATCAACTG 5340
5400 TTCAGGGGCTAGAAATCTGTTGCTATGGGCTTCCACCAATGCTCCACAGATCAACTG 5459
5341 GAATGATGCTACAGCTGTGTTGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5400
5460 GAATGATGCTACAGCTGTGTTGCTTCTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5519
5401 GGCACAGGTGTCCACCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5460
5520 GGCACAGGTGTCCACCAATTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG 5579
5461 TTCCATGCAATTTGGGAGAGTGTGAGGCACTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 5520
5580 TTCCATGCAATTTGGGAGAGTGTGAGGCACTTGTGTTGTTGTTGTTGTTGTTGTTGTTG 5639
5521 AGTGTAGCACTTACCAAGTCCAGAGCTGAGACCTTACCTGATACCCCGAGATCCCCAC 5580
5640 AGTGTAGCACTTACCAAGTCCAGAGCTGAGACCTTACCTGATACCCCGAGATCCCCAC 5699
5581 AGCCACTAC 5589
5700 AGCCACTAC 5708

RESULT 9

US-08-798-691-3
; Sequence 3, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antoinette C.
; APPLICANT: Alvarez, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORMED
; STREET: 200 Perry Parkway
; CITY: Gaithersburg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798,691
; FILING DATE: 12-Feb-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Gallegos
; REGISTRATION NUMBER: 32,692
; REFERENCE/DOCKET NUMBER: PA-0054CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-527-2051
; TELEFAX: 301-208-6997
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: BRCA1
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17
; MAP POSITION: 17q21
; US-08-798-691-3

Query Match 99.9%; Score 5581; DB 1; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5584; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	1	ATGGAATTAATCTGCTCTTGGGTTGAAGAGTACAAAATGTCTATTAATGCTATGCAAAA	60
DB	120	ATGGAATTAATCTGCTCTTGGGTTGAAGAGTACAAAATGTCTATTAATGCTATGCAAAA	179
QY	61	ATCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGCAACTGCTCTCCACAAAGTGTGAC	120
DB	180	ATCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGCAACTGCTCTCCACAAAGTGTGAC	239
QY	121	CACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACAGAGAAAGAGGCTTTCACAG	180
DB	240	CACATATTTTGCATAATTTTGCATGCTGAAACTTCTCAACAGAGAAAGAGGCTTTCACAG	299
QY	181	TGTCCTTTATGTAAGATGATATAACCAAGAGGCTTACAAAGAGTACGAGATTTAGT	240
DB	300	TGTCCTTTATGTAAGATGATATAACCAAGAGGCTTACAAAGAGTACGAGATTTAGT	359
QY	241	CAACTTGTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTTGACACAGGTTTGGAG	300

Db 360 CAACTGTGTGAAGAGCTATTGAAATCATTTGTGCTTTTCAGCTTGAACACAGGTTTGGAG 419
Qy 301 TATGCAACAGCTATAATTTTCCAAAAGAGAAATTAATCTCTCTGACATCTAAAGAT 360
Db 420 TATGCAACAGCTATAATTTTCCAAAAGAGAAATTAATCTCTCTGACATCTAAAGAT 479
Qy 361 GAAGTTTCTATCATCTCAAAGTATGGCTACAGAAACCGTGCCTCAAAAGACTTCTACAGAT 420
Db 480 GAAGTTTCTATCATCTCAAAGTATGGCTACAGAAACCGTGCCTCAAAAGACTTCTACAGAT 539
Qy 421 GAACCGGAAATCTTCTTCAGAGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTGGGA 480
Db 540 GAACCGGAAATCTTCTTCAGAGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTGGGA 599
Qy 481 ACTGTGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTCTGTCTACANT 540
Db 600 ACTGTGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTCTGTCTACANT 659
Qy 541 GAATGGGATCTGATTTCTCTGAGAGATACCGTTAATAGGGAACCTTATGAGTGTGGGA 600
Db 660 GAATGGGATCTGATTTCTCTGAGAGATACCGTTAATAGGGAACCTTATGAGTGTGGGA 719
Qy 601 GATCAAGAAATGTTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGGATTTCT 660
Db 720 GATCAAGAAATGTTTACAAATCACCCCTCAAGGAACCGGATGAATCAGTTTGGATTTCT 779
Qy 661 GCAAAAGGCTGCTGTGAAATTTCTGAGACCGATGTAACAAATATGAAATCATCAA 720
Db 780 GCAAAAGGCTGCTGTGAAATTTCTGAGACCGATGTAACAAATATGAAATCATCAA 839
Qy 721 CCCAGTAATGATTTGAAACCACTCAGAGAGCGTGCAGTGCAGAGGCAATCCAGAAAG 780
Db 840 CCCAGTAATGATTTGAAACCACTCAGAGAGCGTGCAGTGCAGAGGCAATCCAGAAAG 899
Qy 781 TATCAGGATGTTCTGTTTCAAACTTGCATGTGAGGCAATGTGGCACAATACTCATGCC 840
Db 900 TATCAGGATGTTCTGTTTCAAACTTGCATGTGAGGCAATGTGGCACAATACTCATGCC 959
Qy 841 AGCTCATTACAGCATGAGACAGAGTTTATCTCACTAAGACAGAAATGAAATGTAAG 900
Db 960 AGCTCATTACAGCATGAGACAGAGTTTATCTCACTAAGACAGAAATGAAATGTAAG 1019
Qy 901 AAGGCTGAATTTCTGTAATAAAGCAACAGCGCTGGCTTAGCAAGGACCAACATAACAGA 960
Db 1020 AAGGCTGAATTTCTGTAATAAAGCAACAGCGCTGGCTTAGCAAGGACCAACATAACAGA 1079
Qy 961 TGGGCTGGAAGTAGGAAACATGTAATGATAGGCGACTCCAGGCAAGAAAAAGGTA 1020
Db 1080 TGGGCTGGAAGTAGGAAACATGTAATGATAGGCGACTCCAGGCAAGAAAAAGGTA 1139
Qy 1021 GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAAATAGCAAGAACTGCCATGC 1080
Db 1140 GATCTGAATGCTGATCCCTGTGTGAGAGAAAGAAATGGAAATAGCAAGAACTGCCATGC 1199
Qy 1081 TCAGAGAACTCTAGAGATACCTGAAGATGTTCTTGGATTAACCTFAAATAGCAAGATTCAG 1140
Db 1200 TCAGAGAACTCTAGAGATACCTGAAGATGTTCTTGGATTAACCTFAAATAGCAAGATTCAG 1259
Qy 1141 AAGTTAATGAGTGGTTTCCAGAAAGTATGAACTGTTGAGTGTCTGATGATCTCAGATGAT 1200
Db 1260 AAGTTAATGAGTGGTTTCCAGAAAGTATGAACTGTTGAGTGTCTGATGATCTCAGATGAT 1319
Qy 1201 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATTTGAGCGTTCTFAAATAGAGTAGAT 1260
Db 1320 GGGAGTCTGAATCAAAATGCCAAAGTATGATGATTTGAGCGTTCTFAAATAGAGTAGAT 1379
Qy 1261 GAATATTCTGTTCTTCAGAGAAATAGATCTCTGCGGAGTATCTCTCATGAGGCTTTA 1320
Db 1380 GAATATTCTGTTCTTCAGAGAAATAGATCTCTGCGGAGTATCTCTCATGAGGCTTTA 1439
Qy 1321 ATATGTAAGAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATTTGAAGACAAATA 1380

Db 1440 ATATGTAAGAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATTTGAAGACAAATA 1499
Qy 1381 TTTGGGAAACCTTATCGGAGAGGCAAGCTCCCACTTAAGCCATGTAATGTAAT 1440
Db 1500 TTTGGGAAACCTTATCGGAGAGGCAAGCTCCCACTTAAGCCATGTAATGTAAT 1559
Qy 1441 CTAAATATAGGAGCATTTGTTACTGAGCCAAGATTAATCAAGAGCGTCCCTCACAAT 1500
Db 1560 CTAAATATAGGAGCATTTGTTACTGAGCCAAGATTAATCAAGAGCGTCCCTCACAAT 1619
Qy 1501 AAATTAAGGCTTAAGAGGACCTTATCAGGCGCTTATCTCTGAGGATTTTATCAAGAAA 1560
Db 1620 AAATTAAGGCTTAAGAGGACCTTATCAGGCGCTTATCTCTGAGGATTTTATCAAGAAA 1679
Qy 1561 GCAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGAACTAACCAAAOGGAG 1620
Db 1680 GCAGATTTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAGGAACTAACCAAAOGGAG 1739
Qy 1621 CAGAAATGGTCAAGTGAATTAATTAATAGTGGTTCATGAGATTAATAAAGAGTGT 1680
Db 1740 CAGAAATGGTCAAGTGAATTAATTAATAGTGGTTCATGAGATTAATAAAGAGTGT 1799
Qy 1681 TCTAATTCAGAAATGAGAAAAATCTTAACCAATAGAACTACTCGAAAAAGAACTCTGCTTTC 1740
Db 1800 TCTAATTCAGAAATGAGAAAAATCTTAACCAATAGAACTACTCGAAAAAGAACTCTGCTTTC 1859
Qy 1741 AAAACGAAAGCTGAACCTTATAAGCAGCAGTATAAGCAATATGGAATCTCGAAATATC 1800
Db 1860 AAAACGAAAGCTGAACCTTATAAGCAGCAGTATAAGCAATATGGAATCTCGAAATATC 1919
Qy 1801 CACAAATTCAAAAGCAGCTTAAAAAGAAATAGCTGAGGAGAACTCTTCTACAGGCAATTT 1860
Db 1920 CACAAATTCAAAAGCAGCTTAAAAAGAAATAGCTGAGGAGAACTCTTCTACAGGCAATTT 1979
Qy 1861 CATGCCCTTGAATAGTACTAGTGAATTAAGCACTTAAGCCCACTTAATTTGTAATTCGAA 1920
Db 1980 CATGCCCTTGAATAGTACTAGTGAATTAAGCACTTAAGCCCACTTAATTTGTAATTCGAA 2039
Qy 1921 ATTGATAGTGTCTAGCAGTGAAGATTAAGAAATTAAGCACTTAAGCCCACTTAATTTGTA 1980
Db 2040 ATTGATAGTGTCTAGCAGTGAAGATTAAGAAATTAAGCACTTAAGCCCACTTAATTTGTA 2099
Qy 1981 AGSCACAGCAGAAACCTTACAACTCATGGAAGTAAAGAACCTTGCAACTTGAGCCCAAGAG 2040
Db 2100 AGSCACAGCAGAAACCTTACAACTCATGGAAGTAAAGAACCTTGCAACTTGAGCCCAAGAG 2159
Qy 2041 AGTAAACAGCCAAATGGAACAGCAAGATTAAGCAATGACAGTATGATTTTCCAGAGCTG 2100
Db 2160 AGTAAACAGCCAAATGGAACAGCAAGATTAAGCAATGACAGTATGATTTTCCAGAGCTG 2219
Qy 2101 AAGTTAAACAAATGCACTGCTGTTTCTTACTAAGTGTTCATAATACCACTTAAAGAA 2160
Db 2220 AAGTTAAACAAATGCACTGCTGTTTCTTACTAAGTGTTCATAATACCACTTAAAGAA 2279
Qy 2161 TTTGTCAATCTCTAGCCTTCCAAAGAGAAAGAAAGAGAAACTAGAAACAGTTAAAGTG 2220
Db 2280 TTTGTCAATCTCTAGCCTTCCAAAGAGAAAGAAAGAGAAACTAGAAACAGTTAAAGTG 2339
Qy 2221 TCTTAATATGCTGAAGACCCCAAGATCTCACTGTTTAAAGTGAAGAAAGGTTTGCAGAACT 2280
Db 2340 TCTTAATATGCTGAAGACCCCAAGATCTCACTGTTTAAAGTGAAGAAAGGTTTGCAGAACT 2399
Qy 2281 GAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAG 2340
Db 2400 GAAAGATCTGTAGAGAGTAGCAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAG 2459
Qy 2341 GAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGAAAGGCAAAACAGAAATCAA 2400
Db 2460 GAAAGTATCTGTTACTGGAAGTTAGCACTCTAGGAAAGGCAAAACAGAAATCAA 2519
Qy 2401 TGTGTGAGTCAAGTGTGAGCAATTTCAAAACCCCAAGGCACTTAATTCATGTTTCCAAA 2460
Db 2520 TGTGTGAGTCAAGTGTGAGCAATTTCAAAACCCCAAGGCACTTAATTCATGTTTCCAAA 2579

Qy	2461	GATTAATAGAAATGACACAGAGGCGTTTAAAGTATCCATTGGGACATGAAGTTTAAACCAAGT	2520
Db	2580	GATTAATAGAAATGACACAGAGGCGTTTAAAGTATCCATTGGGACATGAAGTTTAAACCAAGT	2639
Qy	2521	CGGGAAAACAAGCATAGAAAATGGAAAGAAATGAACTTGATGCTCAGTATTTTGCAGAAATACA	2580
Db	2640	CGGGAAAACAAGCATAGAAAATGGAAAGAAATGAACTTGATGCTCAGTATTTTGCAGAAATACA	2699
Qy	2581	TTCAAGGTTTCAAAGCCGACAGTCAATTTGCTCTGTTTCAAATCCAGAAAATGCAGAAAGAG	2640
Db	2700	TTCAAGGTTTCAAAGCCGACAGTCAATTTGCTCTGTTTCAAATCCAGAAAATGCAGAAAGAG	2759
Qy	2641	GAATGTGCAACATTTCTCTGCCCATCTCTGGGTCCTTAAAGAAACAAAGTCCCAAAGTCACT	2700
Db	2760	GAATGTGCAACATTTCTCTGCCCATCTCTGGGTCCTTAAAGAAACAAAGTCCCAAAGTCACT	2819
Qy	2701	TTTGAATGTGAACAAAAAGGAAGAAATCAAAGGAAAGAAATCAGTCTAATATCAAGCCCTGTA	2760
Db	2820	TTTGAATGTGAACAAAAAGGAAGAAATCAAAGGAAAGAAATCAGTCTAATATCAAGCCCTGTA	2879
Qy	2761	CAGACAGTTAATATCACTGACAGGCTTTCCTGTGTGGTCGACAGAAATAGGCCAGTTGAT	2820
Db	2880	CAGACAGTTAATATCACTGACAGGCTTTCCTGTGTGGTCGACAGAAATAGGCCAGTTGAT	2839
Qy	2821	AATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGHTTCAGAGGC	2880
Db	2940	AATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGHTTCAGAGGC	2999
Qy	2881	AAGCAAACTGGACTCATTTATCCAAATPAAACATGGACTTTTACAAAACCCATATCGTATA	2940
Db	3000	AAGCAAACTGGACTCATTTATCCAAATPAAACATGGACTTTTACAAAACCCATATCGTATA	3059
Qy	2941	CCACCCTTTTCCCATCAAGTCAATTTGTTTAAAACTAAAAGTAAGAAAATCTGCTAGAG	3000
Db	3060	CCACCCTTTTCCCATCAAGTCAATTTGTTTAAAACTAAAAGTAAGAAAATCTGCTAGAG	3119
Qy	3001	GA AAACTTTGAGAAACATTCAAATGTCACTGAAAGAGAAATGGAAATGAGAACTTTCCA	3060
Db	3120	GA AAACTTTGAGAAACATTCAAATGTCACTGAAAGAGAAATGGAAATGAGAACTTTCCA	3179
Qy	3061	AGTACAGTGAGCAATTAGCCGCTAATAACATTAGAGAAAATGTTTTTAAAGGAGCCAGC	3120
Db	3180	AGTACAGTGAGCAATTAGCCGCTAATAACATTAGAGAAAATGTTTTTAAAGGAGCCAGC	3239
Qy	3121	TTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAAATGAAGTGGGCTCCAGTATTTAATGAA	3180
Db	3240	TTCAAGCAATATTAAATGAAGTAGGTTCCAGTACTAAATGAAGTGGGCTCCAGTATTTAATGAA	3299
Qy	3181	ATAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATTG	3240
Db	3300	ATAGGTTCCAGTGATGAAAACATTTCAAGCAGAACTAGGTAGAAAACAGAGGGCCAAAATTG	3359
Qy	3241	AAATGCTATGCTTAGATTAGGGGTTTTTGCAACCTGAGTCTATAAAACAAAGTCTTCCTGGG	3300
Db	3360	AAATGCTATGCTTAGATTAGGGGTTTTTGCAACCTGAGTCTATAAAACAAAGTCTTCCTGGG	3419
Qy	3301	AGTAAATGTGAAGCATCCTGAAATPAAAAACAAAGNATATGAAGAGTAGTTTCAGACTGTT	3360
Db	3420	AGTAAATGTGAAGCATCCTGAAATPAAAAACAAAGNATATGAAGAGTAGTTTCAGACTGTT	3479
Qy	3361	AATACAGATTTTCTCTCCATATCTGATTTCCAGTAACTTTAGAACAGCCCTATGGGAAGTACT	3420
Db	3480	AATACAGATTTTCTCTCCATATCTGATTTCCAGTAACTTTAGAACAGCCCTATGGGAAGTACT	3539
Qy	3421	CATGCACTCTCAGTTTGTCTGAGACACCTGTAGTACCTGTTAGATGATGGTGAATAAAG	3480
Db	3540	CATGCACTCTCAGTTTGTCTGAGACACCTGTAGTACCTGTTAGATGATGGTGAATAAAG	3599
Qy	3481	GAGATATCTAGTTTTGCTGAAAATGACATTTAAGGAAAGTTCTGCTGTTTTTACGAAAAGC	3540
Db	3600	GAGATATCTAGTTTTGCTGAAAATGACATTTAAGGAAAGTTCTGCTGTTTTTACGAAAAGC	3659

3541	QY	GTCCAGAGAGGAGAGCTTAGCAGAGAGTCTTAGCCCTTTTCACCCATACACATTTGGCTCAG	3600
3660	Db	GTCCAGAAAGGAGAGCTTAGCAGGAGTCTTAGCCCTTTTCACCCATACACATTTGGCTCAG	3719
3601	QY	GTTTACCGAGAGGAGGGCCAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGCAT	3660
3720	Db	GTTTACCGAGAGGAGGGCCAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGCAT	3779
3661	QY	GAAAGGCTTCCCTGCTTCCAAACACTGTTATTTGGTAAAGTAAACAATATACCTTCTCAG	3720
3780	Db	GAAAGGCTTCCCTGCTTCCAAACACTGTTATTTGGTAAAGTAAACAATATACCTTCTCAG	3839
3721	QY	TCTACTAGGCATAGCACGGTGTCTACCGAGTGTCTGCTAAGAACACAGAGGAGAAATTTA	3780
3840	Db	TCTACTAGGCATAGCACGGTGTCTACCGAGTGTCTGCTAAGAACACAGAGGAGAAATTTA	3899
3781	QY	TTATCATTTGAAGATAGCTTTAAATGACTGCGAGTAACACAGGTAAATATTGGCAAGGCATCT	3840
3900	Db	TTATCATTTGAAGATAGCTTTAAATGACTGCGAGTAACACAGGTAAATATTGGCAAGGCATCT	3959
3841	QY	CAGGAACATCACCTTAGTGAGGAAACAAATGTTTCTGCTAGCTTGTTTCTTACAGTGC	3900
3960	Db	CAGGAACATCACCTTAGTGAGGAAACAAATGTTTCTGCTAGCTTGTTTCTTACAGTGC	4019
3901	QY	AGTCAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTCTCTGATTGGTTCT	3960
4020	Db	AGTCAATTTGGAAGACTTGACTGCAAAATACAAACACCCAGGATCCTTCTCTGATTGGTTCT	4079
3961	QY	TCCAAACAAATAGGCGATCAGTCTGAAAGCCAGGAGTGGTCTGAGTGTGACAGGAATTG	4020
4080	Db	TCCAAACAAATAGGCGATCAGTCTGAAAGCCAGGAGTGGTCTGAGTGTGACAGGAATTG	4139
4021	QY	GTTTTCAGATGATGAAGAAAGAGCAACGGCTTCGAAAGAAATATTAACAAGAGAGCAAGC	4080
4140	Db	GTTTTCAGATGATGAAGAAAGAGCAACGGCTTCGAAAGAAATATTAACAAGAGAGCAAGC	4199
4081	QY	ATGGAATTCAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAACAGCGTCTCTGAA	4140
4200	Db	ATGGAATTCAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACAACAGCGTCTCTGAA	4259
4141	QY	GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG	4200
4260	Db	GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATG	4319
4201	QY	CAACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAGCTGTGTTAGAACAG	4260
4320	Db	CAACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACTAGAAGCTGTGTTAGAACAG	4379
4261	QY	CATGGAGCCAGCCCTTCTAAACAGTACCCCTTCATCATAGTGACCTCTTCTGCGCCTTGAG	4320
4380	Db	CATGGAGCCAGCCCTTCTAAACAGTACCCCTTCATCATAGTGACCTCTTCTGCGCCTTGAG	4439
4321	QY	GACTCGGAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCCACAGAAAAGT	4380
4440	Db	GACTCGGAATCCAGAACAAAGCACATCAGAAAAAGCAGTATTAACTTCCACAGAAAAGT	4499
4381	QY	AGTGAATACCCTATAAGCCAGAAATCCAGAGGCCCTTCTGTGTGACAAAGTTGAGGTGTCT	4440
4500	Db	AGTGAATACCCTATAAGCCAGAAATCCAGAGGCCCTTCTGTGTGACAAAGTTGAGGTGTCT	4559
4441	QY	GCAGATAGTTCTACCACTAAATTAAGAACACAGGAGTGAAGGTTCATCCCTCTCTAAA	4500
4560	Db	GCAGATAGTTCTACCACTAAATTAAGAACACAGGAGTGAAGGTTCATCCCTCTCTAAA	4619
4501	QY	TGCCCATCATTAGATAGTGGTACATGCCAGTTGCTCTCTGGAGTCTTCCAGATAGA	4560
4620	Db	TGCCCATCATTAGATAGTGGTACATGCCAGTTGCTCTCTGGAGTCTTCCAGATAGA	4679
4561	QY	AACCTACCCATCTCAAGAGAGCTCATTAGAGTTGTTGATGTGGAGGAGCAACAGCTGGAA	4620
4680	Db	AACCTACCCATCTCAAGAGAGCTCATTAGAGTTGTTGATGTGGAGGAGCAACAGCTGGAA	4739
4621	QY	GAGTCTGGGCCACACCAATTTGACGGAAACATCTTACTTGCCCAAGGCACAGATCTAGAGGA	4680

Db 4740 GAGTCTGGCCACACGATTGACGGAACATCTTACTTTCGCAAGCAGACTCTAGAGGA 4799
Qy 4681 ACCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTCGAATCTGATCTCTCT 4740
Db 4800 ACCCTTACCTGGAATCTGGAATCAGCTCTTCTCTGATGACCTCGAATCTGATCTCTCT 4859
Qy 4741 GAAGCAGAGCCCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4800
Db 4860 GAAGCAGAGCCCGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4919
Qy 4801 AAAGTCTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTGCTGCTGCTG 4860
Db 4920 AAAGTCTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGTCCAGCTGCTGCTGCTGCTGCTG 4979
Qy 4861 GATAGCTGCTGGTATATGCAATGCAAGAGAGAGTGTGAGCAGGAGAGCCAGAGATTGACA 4920
Db 4980 GATAGCTGCTGGTATATGCAATGCAAGAGAGAGTGTGAGCAGGAGAGCCAGAGATTGACA 5039
Qy 4921 GCTTCAACAGAGAGGCTCAACAAAGAGATGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 4980
Db 5040 GCTTCAACAGAGAGGCTCAACAAAGAGATGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5099
Qy 4981 GAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5040
Db 5100 GAATTTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5159
Qy 5041 ACTCAAGAGACTACTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5100
Db 5160 ACTCAAGAGACTACTCAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5219
Qy 5101 CTGAATATTTCTAGGAATTCGCGGAGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5160
Db 5220 CTGAATATTTCTAGGAATTCGCGGAGGAAATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5279
Qy 5161 CAGTCTATTAAAG 5220
Db 5280 CAGTCTATTAAAG 5339
Qy 5221 GTCAATGGAAGAAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5280
Db 5340 GTCAATGGAAGAAACCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5399
Qy 5281 TTCAAGGGCTGAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5340
Db 5400 TTCAAGGGCTGAGAAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5459
Qy 5341 GAATGGAATGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5400
Db 5460 GAATGGAATGCTACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5519
Qy 5401 GGCAAGGTGCTACCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5460
Db 5520 GGCAAGGTGCTACCCCAATTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5579
Qy 5461 TCCATGCAATTTGGGAG 5520
Db 5580 TCCATGCAATTTGGGAG 5639
Qy 5521 AGTGTAGCACTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5580
Db 5640 AGTGTAGCACTTACCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 5699
Qy 5581 AGCCACTAC 5589
Db 5700 AGCCACTAC 5708

RESULT 10

US-08-825-487A-3

; Sequence 3, Application US/08825487A

; Patent No. 6048689

; GENERAL INFORMATION:

; APPLICANT: Murphy, Patricia D.
; APPLICANT: White, Marga B.
; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC
; NUMBER OF SEQUENCES: 110
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howrey & Simon
; STREET: 1299 Pennsylvania Avenue., N.W.
; CITY: Washington,
; STATE: DC
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/825,487A
; FILING DATE: 28-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US98/060002
; FILING DATE: 26-MAR-1998
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Albert P. Halluin
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: 05371.0012.999
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-463-8100
; TELEFAX: 650-463-8400
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: BRCA1
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17
; MAP POSITION: 17q21
; US-08-825-487A-3

Query Match 99.9%; Score 5581; DB 3; Length 5711;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 5584; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 ATGGATTTATCTGCTCTTGGGTTGAGAGTACAAATGTCATTAATGCTATGCAGAAA 60
Db 120 ATGGATTTATCTGCTCTTGGGTTGAGAGTACAAATGTCATTAATGCTATGCAGAAA 179
Qy 61 ATCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGCTCCACAAAGTGTGAC 120
Db 180 ATCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGCTCCACAAAGTGTGAC 239
Qy 121 CACATATTTTGCATAATTTTGCATGCTGAAAATCTTCTCAACCAAGAGAAAGGGCTTCAAG 180
Db 240 CACATATTTTGCATAATTTTGCATGCTGAAAATCTTCTCAACCAAGAGAAAGGGCTTCAAG 299
Qy 181 TGTCTCTTATGTAAGATGATATACCAAGAGGCTTACAAAGAAAGTACGAGATTTAGT 240
Db 300 TGTCTCTTATGTAAGATGATATACCAAGAGGCTTACAAAGAAAGTACGAGATTTAGT 359
Qy 241 CAACTGTGTAGAGCTATGAAAATCATTTTGTGCTTTTGTGCTTGTGACACAGGTTTGAG 300
Db 360 CAACTGTGTAGAGCTATGAAAATCATTTTGTGCTTTTGTGCTTGTGACACAGGTTTGAG 419
Qy 301 TATGCAACAGCTATAATTTTGCATAAGAGAAATTAATCTCTCTGGAACATCTAAAAGAT 360
Db 420 TATGCAACAGCTATAATTTTGCATAAGAGAAATTAATCTCTCTGGAACATCTAAAAGAT 479

361 GAAATTTCTATCATCCAAAGTATCGGCTACAGAAACCGTGCACAAAGACCTCTACAGAGT 420
Db |||||
480 GAAATTTCTATCATCCAAAGTATCGGCTACAGAAACCGTGCACAAAGACCTCTACAGAGT 539
Qy |||||
421 GAAACCCGAAATCTCTCTCTGACGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGA 480
Db |||||
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Qy |||||
481 ACTGTGAGAACTCTGAGGACAAACGCGGATACAACTCAAAAGAGCTGTCTACATTT 540
Db |||||
600 ACTGTGAGAACTCTGAGGACAAACGCGGATACAACTCAAAAGAGCTGTCTACATTT 659
Qy |||||
541 GAATTTGGATCTGATTTCTTCTGAAGATACCGTTTAATAGGCAACTTATTTGAGTGTGGGA 600
Db |||||
660 GAATTTGGATCTGATTTCTTCTGAAGATACCGTTTAATAGGCAACTTATTTGAGTGTGGGA 719
Qy |||||
601 GATCAAGAAATTTTACAAATCAACCTCAAGGACCAAGGATGAATCAGTTTGGATTTCT 660
Db |||||
720 GATCAAGAAATTTTACAAATCAACCTCAAGGACCAAGGATGAATCAGTTTGGATTTCT 779
Qy |||||
561 GCAAAAAGGCTGCTGTGTGAATTTCTGAGACGATGTGAACAAATCTGAACATCATCAA 720
Db |||||
780 GCAAAAAGGCTGCTGTGTGAATTTCTGAGACGATGTGAACAAATCTGAACATCATCAA 839
Qy |||||
721 CCAAGTAAATGAATTTGAACACCACTGAGAGCGTGCACTGAGAGGCAATCCAGAAAG 780
Db |||||
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Db |||||
900 TATCAGGATGTTCTGTTTCAAACTTGCATGTGAGCCATGTGCGCACAAATCTCATGCC 959
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841 AGCTCAATTA CAGATGAGAACAGCAGTTTATTACTCACTAAAGACAGAAATGAATGTAGAA 900
Db |||||
960 AGCTCAATTA CAGATGAGAACAGCAGTTTATTACTCACTAAAGACAGAAATGAATGTAGAA 1019
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Db |||||
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Qy |||||
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Qy |||||
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Db |||||
1920 CACAAATTTCAAAAGCACCTAAAGAAATAGGCTTGAGGAGAACTCTTCTACCGGCAATTT 1979
Qy |||||
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Db |||||
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Db |||||
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Db 2700 TTCAGGTTTCAAAGCGCAGTCAATTTCTCTCTTTTCAAAATCCAGGAAATGCGAGAGAG 2759
Qy 2641 GAATGTGCAACAATCTCTGCCCACTCTCGGTCCTTAAAGAAACAAAGTCCAAAAGTCACT 2700
Db 2760 GAATGTGCAACAATCTCTGCCCACTCTCGGTCCTTAAAGAAACAAAGTCCAAAAGTCACT 2819
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Db |||||
5700 AGCCACTAC 5708

RESULT 11

US-09-074-476-5
; Sequence 5, Application US/09074476
; Patent No. 6130322
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antonette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Thurber, Denise

APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
TITLE OF INVENTION: BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1 (om13)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-09-074-476-5

Query Match 99.9%; Score 5581; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5584; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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DB 1380 GAATATTCTGTTCTTCAGAGAAATAGACTTACTGGCCAGTGTCTCTCATGAGGCTTTA 1439
QY 1321 ATATGTAAGTGAAGAGTTTCACTCCAAATCAGTAGAGTAGATTAATTTGAAGCAAAATA 1380
DB 1440 ATATGTAAGTGAAGAGTTTCACTCCAAATCAGTAGAGTAGATTAATTTGAAGCAAAATA 1499
QY 1381 TTTGGGAAACCTTATCGAGAGGCAAGCTCCCAACTTAAGCCATGTAACTGAAAT 1440
DB 1500 TTTGGGAAACCTTATCGAGAGGCAAGCTCCCAACTTAAGCCATGTAACTGAAAT 1559
QY 1441 CTAATATAGGAGCATTTGTTTACTGAGCCACAGATATCAAGAGCGTCCCTCCACAAAT 1500

DB 1560 CTAATATAGGAGCATTTGTTTACTGAGCCACAGATAATAAAGAGCGTCCCTCCACAAAT 1619
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DB 1620 AAATTAAGCGTAAAAAGGAGAGCTCATCAGGCTTTCATCTCCTGAGGATTTTATCAAGAAA 1679
QY 1561 GCAGATTTGGCAGTTCCAAAGACTCTCGAAATGATTAATCAGGGAACTAACCAACGGAG 1620
DB 1680 GCAGATTTGGCAGTTCCAAAGACTCTCGAAATGATTAATCAGGGAACTAACCAACGGAG 1739
QY 1621 CAGAAATGGTCAAGTGTGATTAATTAATAGTGTGTCATGAGAAATAAAACAAAGGTGAT 1680
DB 1740 CAGAAATGGTCAAGTGTGATTAATTAATAGTGTGTCATGAGAAATAAAACAAAGGTGAT 1799
QY 1681 TCTATTTCAGAAATGAGAAAAATCTAACCCAAATAGAAATCACTCGAAAAAGAAATCTGCTTTC 1740
DB 1800 TCTATTTCAGAAATGAGAAAAATCTAACCCAAATAGAAATCACTCGAAAAAGAAATCTGCTTTC 1859
QY 1741 ARAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGAACTCGAAATTTAAATATC 1800
DB 1860 ARAACGAAAGCTGAACCTTATAGCAGCAGTATAAGCAATATGAACTCGAAATTTAAATATC 1919
QY 1801 CCAATTTCAAAAGCACCTTAAAGAAATAGGCTGAGGAGGAACTCTTCTACAGGCAATT 1860
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QY 2341 GAAAGATCTGTAGAGTAGCAGTATTCATTTGGTACTCTGTTACTGATTTAGCTCAG 2400
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QY 2521 CGGGAAAACAGCATGAGAAATGGAAGAAAGTGAATGATGCTCAGTATTTGAGAAATACA 2580

4741 GAAGACAGAGCCCGAGAGTCACTGCTGGTGGCAACATACCATCTTCAACCTCTGCATTG 4800
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4860 GAAGACAGAGCCCGAGAGTCACTGCTGGTGGCAACATACCATCTTCAACCTCTGCATTG 4919
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Qy 5581 AGCCACTAC 5589
Db 5700 AGCCACTAC 5708

RESULT 12

US-08-658-322-1
; Sequence 1, Application US/08658322
; Patent No. 5869245
; GENERAL INFORMATION:
; APPLICANT: Yeung, Anthony T.
; TITLE OF INVENTION: Mismatch Endonuclease And Its Use in
; IDENTIFYING MUTATIONS IN TARGETED POLYNUCLEOTIDE STRANDS
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dann, Dorfman, Herrell and Skillman, P.C.
; STREET: 1601 Market Street, Suite 720

CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103-2307
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/658,322
FILING DATE: 05-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hagan, Patrick J.
REGISTRATION NUMBER: 27,643
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 563-4100
TELEFAX: (215) 563-4044
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: not relevant
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-658-322-1

Query Match 99.8%; Score 5579.4; DB 2; Length 5711;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 5583; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGAGTTTATCTCTCTCTCGCTGGAAGAGTACAAATGTCTATTAATCTATGCGAAA 60

Db 120 ATGAGTTTATCTCTCTCTCGCTGGAAGAGTACAAATGTCTATTAATCTATGCGAAA 179

Qy 61 ATCTAGAGTGTCCATCTCTGAGTTGATCAAGGACCTGTCTCCCAAGGTGTGAC 120

Db 180 ATCTAGAGTGTCCATCTCTGAGTTGATCAAGGACCTGTCTCCCAAGGTGTGAC 239

Qy 121 CACATATTTTGCAAAATTTTGCAATGCTGTAACCTTCTCAACAGAGAAAGGCTTACAG 180

Db 240 CACATATTTTGCAAAATTTTGCAATGCTGTAACCTTCTCAACAGAGAAAGGCTTACAG 299

Qy 181 TGTCTTTATGTAAGATGATTAACCAAGAGAGCTTACCAAGAGTACAGATTTAGT 240

Db 300 TGTCTTTATGTAAGATGATTAACCAAGAGAGCTTACCAAGAGTACAGATTTAGT 359

Qy 241 CAACTTGTGGAAGAGCTATTGAAATTCATTTGTGCTTTTTCAGCTTGACACAGTTTGGAG 300

Db 360 CAACTTGTGGAAGAGCTATTGAAATTCATTTGTGCTTTTTCAGCTTGACACAGTTTGGAG 419

Qy 301 TATGCAACAGCTATAATTTTGCAGAAAGGAAATTAATCTCTCTGAGACATCTAAAGAT 360

Db 420 TATGCAACAGCTATAATTTTGCAGAAAGGAAATTAATCTCTCTGAGACATCTAAAGAT 479

Qy 361 GAAGTTTCTATCATCCAAAGTATGCTACAGAACCTGCGCAAGAGCTTCTACAGAGT 420

Db 480 GAAGTTTCTATCATCCAAAGTATGCTACAGAACCTGCGCAAGAGCTTCTACAGAGT 539

Qy 421 GAACCGAAATCTCTCTGAGGAAACCACTCTCAGTGTCCAATCTCTTAACCTTGA 480

Db 540 GAACCGAAATCTCTCTGAGGAAACCACTCTCAGTGTCCAATCTCTTAACCTTGA 599

Qy 481 ACTGTGAGAGCTCTGAGGAGCAAGGAGTACAACTCAAGAGAGCTCTGTCTACATT 540

Db 600 ACTGTGAGAGCTCTGAGGAGCAAGGAGTACAACTCAAGAGAGCTCTGTCTACATT 659

Qy 541 GAATGGGATCTGATTTCTCTGAGATACCGTTAATAAGGCACTTATTGCAAGTGTGGA 600

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840 CCAGTAATGAATGTTGAACACCACTGAGAACGCTGACGTGAGAGGCATCCAGAAAG 899
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Db
4680 AACTACCCATCTCAAGAGGAGCTCAATTAAGTGTGTTGATGTCGAGGAGCAACAGCTGGA 4739
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Db
4740 GAGTCTGGGCCACACGATTTGACGGAACATCTTACTTCCAGGCAAGGATCTAGAGGA 4799
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4681 ACCCTTACTCTGAAATCTGGAATCAGCTCTTCTCTGATGACCTGAAATCTGATCTTCT 4740
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4920 AAGTTTCCCAATTTCAAGTTTCAGAACTGCCCCAGAGTCCAGGCTGCTCTCATACTACT 4979
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4861 GATACCTGCTGGGTATAATGCAATGGAAGAAAGTGTGAGCAGGAGAACCCAGAAATTGACA 4920
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DB 5640 AGTGTAGCACTTACAG 5699
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DB 5700 AGCACTAC 5708

RESULT 13

US-08-603-753D-1
; Sequence 1, Application US/08603753D
; Patent No. 5891857
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: SZABO, CSILLA I.
; APPLICANT: JETTON, THOMAS L.
; APPLICANT: ROBINSON-BENSON, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
; STREET: BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kB storage

COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.11
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5712
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: ductal carcinoma in situ, invasive
CELL TYPE: breast cancer and normal breast tissue
CELL LINE: not derived from a cell line
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA1
LOCATION: GenBank accession no. U14680
IDENTIFICATION METHOD: microscopically directed
IDENTIFICATION METHOD: sampling and nuclease protection assay
OTHER INFORMATION: gene encoding BRCA1 protein
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 1:
US-08-603-753D-1

Query Match 99.8%; Score 5579.4; DB 2; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5583; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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DB 120 ATGGATTTATCTGCTCTCGGTTGAGAGAGTACAAATGTCATTAATGCTATGCGAGAA 179
QY 61 ATCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGCTCCACAAGTGTGAC 120
DB 180 ATCTTAGAGTGTCCCATCTGCTGAGTGTGATCAAGGAACCTGCTCCACAAGTGTGAC 239
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Db 360 CAATCTGTTGAAGAGCTATTCGAATCATTTGTGCTTTTTCAGCTGTGACACAGGTTTCGAG 419
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Db 420 TATGCAAAACAGCTATAATTTTGCAAAAAGGAAATAAATCTCTCTGACATCTCAAAAGAT 479
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Qy 601 GATCAAGAAATGTTTACAAATCAACCCCTCAAGAAACCAAGGATGAAATCAGTTTGGATTTCT 660
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Qy 721 CCCAGTAATATGATTTGAACACCACTGAGAGCGTGCAGCTGAGAGGCAATCCAGAAAG 780
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Qy 1321 ATATGTAAAGTGTGAAGGTTCACTCCAAATCAGTAGAGAGTATATTTGAAGCAAAATA 1380
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Qy 5341 GAATGATGTTGACAGCTGTGTGCTCTCTGTGTGAGGAGCTTTCATCATTCACCCCTT 5400
Db 5460 GAATGATGTTGACAGCTGTGTGCTCTCTGTGTGAGGAGCTTTCATCATTCACCCCTT 5519
Qy 5401 GGCAAGAGTGTCCACCCCAATTTGGTGTGAGCCAGATGCTGGAAGAGGCAATGGC 5460
Db 5520 GGCAAGAGTGTCCACCCCAATTTGGTGTGAGCCAGATGCTGGAAGAGGCAATGGC 5579
Qy 5461 TTCCATGCAATTTGGGACAGATGTTGAGGACCTGTGGTACCCAGAGTGGTGTGGAC 5520
Db 5580 TTCCATGCAATTTGGGACAGATGTTGAGGACCTGTGGTACCCAGAGTGGTGTGGAC 5639
Qy 5521 AGTGTAGCACTCTACCAAGTCCAGGAGTGGACACCTTACCTGATACCCAGATCCCCAC 5580
Db 5640 AGTGTAGCACTCTACCAAGTCCAGGAGTGGACACCTTACCTGATACCCAGATCCCCAC 5699
Qy 5581 AGCCACTAC 5589
|||||

Db 5700 AGCCACTAC 5708
RESULT 14
US-09-099-753-1
; Sequence 1, Application US/09099753
; Patent No. 614903
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: PAGE, DAVID L.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: SZABO, CSILLA I.
; APPLICANT: JETTON, THOMAS L.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
; TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
; TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ARLES A. TAYLOR, JR.
; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
; STREET: BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 800 kB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/099,753
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/603,753
; FILING DATE: 20 FEB 1996
; APPLICATION NUMBER: U.S. 08/373,799
; FILING DATE: 17 JAN 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/2
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; TELEX:
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5712
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: no
; ANTI-SENSE: no
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; INDIVIDUAL ISOLATE:
; DEVELOPMENTAL STAGE: adult
; TISSUE TYPE: female breast
; CELL TYPE: ductal carcinoma in situ, invasive
; CELL TYPE: breast cancer and normal breast tissue
; CELL LINE: not derived from a cell line
; ORGANELLS: no
; IMMEDIATE SOURCE:
; LIBRARY: cDNA library derived from human
; CLONE: obtained using published sequence
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: unknown

MAP POSITION: unknown
UNITS: unknown
FEATURE: unknown
NAME/KEY: BRCA1
LOCATION: GenBank accession no. U14680
IDENTIFICATION METHOD: microscopically directed
IDENTIFICATION METHOD: sampling and nuclease protection assay
OTHER INFORMATION: gene encoding BRCA1 protein
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 1:
US-09-099-753-1

Query Match 99.8%; Score 5579.4; DS 3; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5583; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 ATGGATTATCTGCTCTCTCGGTTGAAGAGTACAAATGTCAATTAATGCTATGCGAGAAA 60
Db 120 ATGGATTATCTGCTCTCTCGGTTGAAGAGTACAAATGTCAATTAATGCTATGCGAGAAA 179

Qy 61 ATCTTAGAGTCTCCATCTGCTGGAGTTGATCAAGAACTGTCTCCACAAAGTGTGAC 120
Db 180 ATCTTAGAGTCTCCATCTGCTGGAGTTGATCAAGAACTGTCTCCACAAAGTGTGAC 239

Qy 121 CACATATTTTGCATGCTGAACTTCTCAACGAGAAAGAGGCGCTTCCACAG 180
Db 240 CACATATTTTGCATGCTGAACTTCTCAACGAGAAAGAGGCGCTTCCACAG 299

Qy 181 TGCTCTTATCTAGAGATGATATACCAAGAGGAGCTCAAGAAAGTACGAGATTAGT 240
Db 300 TGCTCTTATCTAGAGATGATATACCAAGAGGAGCTCAAGAAAGTACGAGATTAGT 359

Qy 241 CAATCTTGTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGAACAGGTTGGAG 300
Db 360 CAATCTTGTGAAGAGCTATTGAAATCAATTTGTGCTTTTTCAGCTTGAACAGGTTGGAG 419

Qy 301 TATGCAACAGCTATATTTTGCAAAAGGAAATTAATCTCTGAACTCTAAGAT 360
Db 420 TATGCAACAGCTATATTTTGCAAAAGGAAATTAATCTCTGAACTCTAAGAT 479

Qy 361 GAAGTTTCTATCTATCCAAAGTATGGGCTACAGAAAACCGTGCCAAAAGACTTCTACAGAT 420
Db 480 GAAGTTTCTATCTATCCAAAGTATGGGCTACAGAAAACCGTGCCAAAAGACTTCTACAGAT 539

Qy 421 GAACCGAAATCTCTCTTGGAGGAAACCGAGTCTAGTGTCAACTCTCTAACTTTGGA 480
Db 540 GAACCGAAATCTCTCTTGGAGGAAACCGAGTCTAGTGTCAACTCTCTAACTTTGGA 599

Qy 481 ACTGTGAGAACTCTGAGCAAAAGCAGCGATCAACCTCAAAAGAGCTCTGTCTACATT 540
Db 600 ACTGTGAGAACTCTGAGCAAAAGCAGCGATCAACCTCAAAAGAGCTCTGTCTACATT 659

Qy 541 GAATTTGGATCTGATCTTCTGAGATACCGTTTAATAAGGCACTTATTGCAAGTGGGA 600
Db 660 GAATTTGGATCTGATCTTCTGAGATACCGTTTAATAAGGCACTTATTGCAAGTGGGA 719

Qy 601 GATCAGAATTTGTACAAATCAACCTCAAGGAACGAGGATCAATTCAGTTGGATTCT 660
Db 720 GATCAGAATTTGTACAAATCAACCTCAAGGAACGAGGATCAATTCAGTTGGATTCT 779

Qy 661 GCAAAAAGGCTGCTGTGTAATTTCTGACACGGATGTAAACAAATCTGAAACATCAAA 720
Db 780 GCAAAAAGGCTGCTGTGTAATTTCTGACACGGATGTAAACAAATCTGAAACATCAAA 839

Qy 721 CCCAGTAATGATTTTGAACACCACTGAGAAAGCGGTGAGGAGGAGTCTTCTACAGGATAT 780

Db 840 CCCAGTAATGATTTTGAACACCACTGAGAAAGCGGTGAGGAGGAGTCTTCTACAGGATAT 899

Qy 781 TATCAGGTTAGTTCTGTTTCAAACTTGGCATGTGGAGCCATGTGGCAAAATCTCATGCC 840
Db 900 TATCAGGTTAGTTCTGTTTCAAACTTGGCATGTGGAGCCATGTGGCAAAATCTCATGCC 959

Qy 841 AGCTCATTTACAGCATGAGAACAGCAGTTTATTTACTCACTAAAGCAGAAATGTAAGAA 900
Db 960 AGCTCATTTACAGCATGAGAACAGCAGTTTATTTACTCACTAAAGCAGAAATGTAAGAA 1019

Qy 901 AAGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTAGCAAGGAGCCAACTAATACAGA 960
Db 1020 AAGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTAGCAAGGAGCCAACTAATACAGA 1079

Qy 961 TGGGCTGGAAGTAAAGAAACATGTATGATAGGCGGACTCCAGCAGCAGAAAAGGTA 1020
Db 1080 TGGGCTGGAAGTAAAGAAACATGTATGATAGGCGGACTCCAGCAGCAGAAAAGGTA 1139

Qy 1021 GATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAAGCAGAAACTGCCATGC 1080
Db 1140 GATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAAGCAGAAACTGCCATGC 1199

Qy 1081 TCAGAGATCTTAGAGATCTGAAGATGTTCTTGGATTAACACTAATAGCAGCATTCAG 1140
Db 1200 TCAGAGATCTTAGAGATCTGAAGATGTTCTTGGATTAACACTAATAGCAGCATTCAG 1259

Qy 1141 AAAGTTAATGAGTGGTTTTCAGAGTGTGAATCTGTAGGTTCTGATGACTCAGCATGAT 1200
Db 1260 AAAGTTAATGAGTGGTTTTCAGAGTGTGAATCTGTAGGTTCTGATGACTCAGCATGAT 1319

Qy 1201 GGGAGTCTGAATCAAAATGCCAAAGTGTGATTAATGGAGCTTTCTAAATGAGGTAGAT 1260
Db 1320 GGGAGTCTGAATCAAAATGCCAAAGTGTGATTAATGGAGCTTTCTAAATGAGGTAGAT 1379

Qy 1261 GAATATTTCTGTTTCTTTCAGAGAAAATAGACTTACTGGCCAGTGTCTCATGAGGCTTTA 1320
Db 1380 GAATATTTCTGTTTCTTTCAGAGAAAATAGACTTACTGGCCAGTGTCTCATGAGGCTTTA 1439

Qy 1321 ATATGTAAAGTGAAGAGTTCACTCCAATCAGTAGAGAGTAATAATTGAAGCAAAATA 1380
Db 1440 ATATGTAAAGTGAAGAGTTCACTCCAATCAGTAGAGAGTAATAATTGAAGCAAAATA 1499

Qy 1381 TTTGGGAAAACCTATCGGAAGAGGCAAGCTCCCACTTAAGCCATCTTAAGTAAAT 1440
Db 1500 TTTGGGAAAACCTATCGGAAGAGGCAAGCTCCCACTTAAGCCATCTTAAGTAAAT 1559

Qy 1441 CTAAATATAGGAGCAATTTGTTACTGAGCCACAGATAATAAGAGCGTCCCTCACAAT 1500
Db 1560 CTAAATATAGGAGCAATTTGTTACTGAGCCACAGATAATAAGAGCGTCCCTCACAAT 1619

Qy 1501 AAATTAAGCGTAAAGAGACCTACATCAGGCTTTCATCTGAGGATTTTATCAGAAA 1560
Db 1620 AAATTAAGCGTAAAGAGACCTACATCAGGCTTTCATCTGAGGATTTTATCAGAAA 1679

Qy 1561 GCAGATTTGGCAGTTTCAAAAGACTCTGAAATGATAAATCAGGAACTTAACCAACGGAG 1620
Db 1680 GCAGATTTGGCAGTTTCAAAAGACTCTGAAATGATAAATCAGGAACTTAACCAACGGAG 1739

Qy 1621 CAGATGTTCAAGTCAATGAATTAATTAATAGTGTCTAGAGATAAACAACAAAGGTGAT 1680
Db 1740 CAGATGTTCAAGTCAATGAATTAATTAATAGTGTCTAGAGATAAACAACAAAGGTGAT 1799

Qy 1681 TCTATTTCAAGATGAGAAAATCTTAACCCCAATAGAACTCACTGAAAAGAAATCTCTTTC 1740
Db 1800 TCTATTTCAAGATGAGAAAATCTTAACCCCAATAGAACTCACTGAAAAGAAATCTCTTTC 1859

Qy 1741 AAAACGAAAGCTGAACCTTAAAGCAGCAGTAAAGCAATATGGAATCTGAAATTAATATC 1800
Db 1860 AAAACGAAAGCTGAACCTTAAAGCAGCAGTAAAGCAATATGGAATCTGAAATTAATATC 1919

Qy 1801 CCAATTTCAAGACCTTAAAGAGATAGGCTGAGGAGAGTCTTCTTACAGGAGATAT 1860
Db 1920 CCAATTTCAAGACCTTAAAGAGATAGGCTGAGGAGAGTCTTCTTACAGGAGATAT 1979

1861 QY CATGGCTTGAACCTAGTAGTCAGTAGAAATCTAAGCCCACTAAATGCTACTGAAATGCCAA 1920
1980 Db CATGGCTTGAACCTAGTAGTCAGTAGAAATCTAAGCCCACTAAATGCTACTGAAATGCCAA 2039
1921 QY ATTGATAGTGTCTTACGAGTGAAGATGAAGAAAGAAAGTACCAACCAATGCCAGTC 1980
2040 Db ATTGATAGTGTCTTACGAGTGAAGATGAAGAAAGAAAGTACCAACCAATGCCAGTC 2099
1981 QY AGGCACAGCAAAACCTACAACTCATGGAAGGTAAAGAACTGCACTGGAGGCCAAG 2040
2100 Db AGGCACAGCAAAACCTACAACTCATGGAAGGTAAAGAACTGCACTGGAGGCCAAG 2159
2041 QY AGTACAGCCCAATGACAGCAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2100
2160 Db AGTACAGCCCAATGACAGCAAGTAAAGACATGACAGTGTATCTTTCCAGAGCTG 2219
2101 QY AAGTTAAACAAATGCACCTGTGTTCTTTTACTAAGTGTTCAAATACCACTGAACTTAAAGAA 2160
2220 Db AAGTTAAACAAATGCACCTGTGTTCTTTTACTAAGTGTTCAAATACCACTGAACTTAAAGAA 2279
2161 QY TTGTGCAATCTAGCTTCCAGAGAGAGAAAGAGAGAACTAGAAACAGTTAAAGTG 2220
2280 Db TTGTGCAATCTAGCTTCCAGAGAGAGAAAGAGAGAACTAGAAACAGTTAAAGTG 2339
2221 QY TCTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCRAACT 2280
2340 Db TCTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCRAACT 2399
2281 QY GAAAGATCTGAGAGATGAGCAGTATTTCACTGTGTACTGTGTACTGATTTGGCAGCTCAG 2340
2400 Db GAAAGATCTGAGAGATGAGCAGTATTTCACTGTGTACTGTGTACTGATTTGGCAGCTCAG 2459
2341 QY GAAAGATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATATAA 2400
2460 Db GAAAGATCTGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGAACCAATATAA 2519
2401 QY TGTGTAGTCACTGTGAGCAATTTGAAACCCCAAGGCACTAAATCATGTTGTTCCAAA 2460
2520 Db TGTGTAGTCACTGTGAGCAATTTGAAACCCCAAGGCACTAAATCATGTTGTTCCAAA 2579
2461 QY GATTAAGATGACACAGAGGCTTTAAGTATCCATGAGACATGAAGTTAACCACT 2520
2580 Db GATTAAGATGACACAGAGGCTTTAAGTATCCATGAGACATGAAGTTAACCACT 2639
2521 QY CGGGAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAAGTATTTGCAATACA 2580
2640 Db CGGGAACAAGCATAGAAATGGAAGAAAGTGAACCTTGATGCTCAAGTATTTGCAATACA 2699
2581 QY TTCAAGGTTTCAAGCCGCACTATTTGCTCTGTTTCAAAATCCAGGAATGCAAGAG 2640
2700 Db TTCAAGGTTTCAAGCCGCACTATTTGCTCTGTTTCAAAATCCAGGAATGCAAGAG 2759
2641 QY GAATGTGCAATTTCTGTCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACT 2700
2760 Db GAATGTGCAATTTCTGTCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACT 2819
2701 QY TTGGAATGTGAACAAAAGGAAGAAATCAAGGAAGAAATGAGTCTAATATCAAGCCCTGTA 2760
2820 Db TTGGAATGTGAACAAAAGGAAGAAATCAAGGAAGAAATGAGTCTAATATCAAGCCCTGTA 2879
2761 QY CAGACAGTTAATATCACTGCAAGGCTTCTGTTGTTGTCAGGAAGATGAAGCCAGTTGAT 2820
2880 Db CAGACAGTTAATATCACTGCAAGGCTTCTGTTGTTGTCAGGAAGATGAAGCCAGTTGAT 2939
2821 QY AATGCCAATGATATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 2880
2940 Db AATGCCAATGATATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGC 2999
2881 QY AACGAACTGACCTACTTACCTCAAAATGAACATGAGCTTTTACAAAACCCATATCGTATA 2940
3000 Db AACGAACTGACCTACTTACCTCAAAATGAACATGAGCTTTTACAAAACCCATATCGTATA 3059

2941 QY CACGACTTTTCCGATCAAGTCAATTTGTTAAAACTAATGTAAAGAAAAATCTGCTAGAG 3000
3060 Db CACGACTTTTCCGATCAAGTCAATTTGTTAAAACTAATGTAAAGAAAAATCTGCTAGAG 3119
3001 QY GAAACCTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGAAATCAGAACATTTCCA 3060
3120 Db GAAACCTTTGAGGAACATTTCAATGTCACTGAAAGAGAAATGGAAATCAGAACATTTCCA 3179
3061 QY AGTACAGTGAAGCAAAATTAGCCGTAATATACATTAGAGAAATTTGTTTAAAGAGGAGCC 3120
3180 Db AGTACAGTGAAGCAAAATTAGCCGTAATATACATTAGAGAAATTTGTTTAAAGAGGAGCC 3239
3121 QY TCAAGCAATATTAATGAAGTAGTTCCTACTACTTAATGAAGTGGCTCCAGTATTTAATGAA 3180
3240 Db TCAAGCAATATTAATGAAGTAGTTCCTACTACTTAATGAAGTGGCTCCAGTATTTAATGAA 3299
3181 QY ATAGTTCAGTGAATGAACAACTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTG 3240
3300 Db ATAGTTCAGTGAATGAACAACTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAATTTG 3359
3241 QY AATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTATAACAAAGTCTTCTCGA 3300
3360 Db AATGCTATGCTTAGATTAGGGGTTTTGCAACCTGAGGCTCTATAACAAAGTCTTCTCGA 3419
3301 QY AGTAAATTGTAAGCATCTCGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTT 3360
3420 Db AGTAAATTGTAAGCATCTCGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTT 3479
3361 QY AATACAGATTTCTCTCATATCTGATTTAGATTAAGTACAGTCTATGGAAGTCTTCTCGA 3420
3480 Db AATACAGATTTCTCTCATATCTGATTTAGATTAAGTACAGTCTATGGAAGTCTTCTCGA 3539
3421 QY CATGCACTCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG 3480
3540 Db CATGCACTCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATGGTGAATAAAG 3599
3481 QY GAAGTACTAGTTTCTGCGAAATGAACATTAAGGAAGTCTGCTGTTTGTAGCAAAAGC 3540
3600 Db GAAGTACTAGTTTCTGCGAAATGAACATTAAGGAAGTCTGCTGTTTGTAGCAAAAGC 3659
3541 QY GTCCAGAGAGGAGGCTTAGCAGGAGTCTTAGCCCTTTTCCACCATACACATTTGGCTCAG 3600
3660 Db GTCCAGAGAGGAGGCTTAGCAGGAGTCTTAGCCCTTTTCCACCATACACATTTGGCTCAG 3719
3601 QY GGTACCGAAGAGGGGCCAAGAAAATTAGAGTCTCTAGAGAGAGAACTTATCTAGTAGGAT 3660
3720 Db GGTACCGAAGAGGGGCCAAGAAAATTAGAGTCTCTAGAGAGAGAACTTATCTAGTAGGAT 3779
3661 QY GAAGAGCTTCCCTGCTTCCAACTTTGTTTAAAGTAAACAAATATACCTTCTCAG 3720
3780 Db GAAGAGCTTCCCTGCTTCCAACTTTGTTTAAAGTAAACAAATATACCTTCTCAG 3839
3721 QY TCTACTAGGCATAGCAACCTTGTCTACCGAGTGTCTGTCTAAGAACACAGAGGAAATTTA 3780
3840 Db TCTACTAGGCATAGCAACCTTGTCTACCGAGTGTCTGTCTAAGAACACAGAGGAAATTTA 3899
3781 QY TTATCAATTGAGATAGCTTTAATGCTGACGTACCAAGGTAATATTTGCAAGGATCT 3840
3900 Db TTATCAATTGAGATAGCTTTAATGCTGACGTACCAAGGTAATATTTGCAAGGATCT 3959
3841 QY CAGGAACATCACCTTAGTGAGGAAAACAAATGTTCTGTAGCTGTGTTTCTTCCAGAGTC 3900
3960 Db CAGGAACATCACCTTAGTGAGGAAAACAAATGTTCTGTAGCTGTGTTTCTTCCAGAGTC 4019
3901 QY AGTGAATTGGAAGACTTTGACTGCAATAAACAACCCAGGATCTTCTTGTGTTCT 3960
4020 Db AGTGAATTGGAAGACTTTGACTGCAATAAACAACCCAGGATCTTCTTGTGTTCT 4079
3961 QY TCCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCAGAGGAATTTG 4020
4080 Db TCCAAAACAAATGAGGATCAGTCTGAAAGCCAGGAGTTGGTCTGAGTGCAGAGGAATTTG 4139
4021 QY GTTTCAGATGATGAAGAAAGAGAAACGGGCTTGGAGAGAAAAATATCAAGAGAGCAAGC 4080

Db 4140 GTTTCAGATGTCAGAGAGAGAGAAACGGCTTUGAAGAAATTAATCAAGAGAGCAAGC 4199
Qy 4081 ATGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCGTCTCTGAA 4140
Db 4200 ATGGATTCAAACTTAGGTGAAGCAGCATCTGGGTGTGAGAGTGAACCAAGCGTCTCTGAA 4259
Qy 4141 GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTAAACCACTCAGCAGAGGGATACCATG 4200
Db 4260 GACTGCTCAGGGCTATCCTCTCAGAGTGACATTTAAACCACTCAGCAGAGGGATACCATG 4319
Qy 4201 CAACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAG 4260
Db 4320 CAACATAACCTGATAAAGCTCCAGCAGGAAATGGCTGAACCTAGAGCTGTGTAGAACAG 4379
Qy 4261 CATGGAGCCAGCCTTCTAACAGCTACCTTCCATCATAGTGACTCTTCTGCCCCTTGAG 4320
Db 4380 CATGGAGCCAGCCTTCTAACAGCTACCTTCCATCATAGTGACTCTTCTGCCCCTTGAG 4439
Qy 4321 GACTCGGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGTATTACTTCAAGAAAACT 4380
Db 4440 GACTCGGAAATCCAGAACAAAGCAGCATCAGAAAAAGCAGTATTACTTCAAGAAAACT 4499
Qy 4381 AGTGAATACCTTATAAGCCAGAAATCAGAAAGGCTTCTCTGAGCAAGTTTGAAGGTCT 4440
Db 4500 AGTGAATACCTTATAAGCCAGAAATCAGAAAGGCTTCTCTGAGCAAGTTTGAAGGTCT 4559
Qy 4441 GCAGATAGTCTACCAAGTAAATAAAGAACACAGGAGTGCAAGGTCTCCCTCTTAA 4500
Db 4560 GCAGATAGTCTACCAAGTAAATAAAGAACACAGGAGTGCAAGGTCTCCCTCTTAA 4619
Qy 4501 TGCCCAATCATAGATAGGTGGTACATGCAAGTTGCTCTGGAGTCTTCAGAAATAGA 4560
Db 4620 TGCCCAATCATAGATAGGTGGTACATGCAAGTTGCTCTGGAGTCTTCAGAAATAGA 4679
Qy 4561 AACTACCCATCTCAAGCAGAGCTCATTAAAGTGTGTGATGTGGAGGAGCAAGCTGGAA 4620
Db 4680 AACTACCCATCTCAAGCAGAGCTCATTAAAGTGTGTGATGTGGAGGAGCAAGCTGGAA 4739
Qy 4621 GAGTCTGGGCCACACGATTGTGCGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGA 4680
Db 4740 GAGTCTGGGCCACACGATTGTGCGAAACATCTTACTTCCCAAGGCAAGATCTAGAGGA 4799
Qy 4681 ACCCTTACTCGGATCTGGAATCAGCCTTCTCTGATGACCCCTGAATCTGATCCTCT 4740
Db 4800 ACCCTTACTCGGATCTGGAATCAGCCTTCTCTGATGACCCCTGAATCTGATCCTCT 4859
Qy 4741 GAAGCAGAGCCCCAGAGTCAGTCTGTGTGGCAACATACCATCTTCAACCTCTGCATTG 4800
Db 4860 GAAGCAGAGCCCCAGAGTCAGTCTGTGTGGCAACATACCATCTTCAACCTCTGCATTG 4919
Qy 4801 AAAGTTCGCCAATTTGAAGTTGAGATCTGCCAGGCTCCAGCTGCTGCTCATACTACT 4860
Db 4920 AAAGTTCGCCAATTTGAAGTTGAGATCTGCCAGGCTCCAGCTGCTGCTCATACTACT 4979
Qy 4861 GATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCCAGAAATGACA 4920
Db 4980 GATACTGCTGGGTATATGCAATGGAAGAAAGTGTGAGCAGGAGGAGCCAGAAATGACA 5039
Qy 4921 GCTTCAACAGAAAGGCTCAACAAAAGATGTCTGAGTGTGTCTGGCTGACCCCGAGAA 4980
Db 5040 GCTTCAACAGAAAGGCTCAACAAAAGATGTCTGAGTGTGTCTGGCTGACCCCGAGAA 5099
Qy 4981 GAATTTGCTGCTGTAGAGTTTCCAGAAACACCAATCACTTAACTAATCTAAT 5040
Db 5100 GAATTTGCTGCTGTAGAGTTTCCAGAAACACCAATCACTTAACTAATCTAAT 5159
Qy 5041 ACTGAAGAGACTACTCATGTTGTATGAAAAAGATGCTGAGTTGTGTGAGAGGACA 5100
Db 5160 ACTGAAGAGACTACTCATGTTGTATGAAAAAGATGCTGAGTTGTGTGAGAGGACA 5219
Qy 5101 CTGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTCTTGGGTGACC 5160

Db 5220 CTGAATATTTCTAGGAATTCGGGAGGAAATGGGTAGTTAGCTATTCTTGGGTGACC 5279
Qy 5161 CAGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTG 5220
Db 5280 CAGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGAGATGTG 5339
Qy 5221 GTCAATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGATCCAGAGACAGAAAGATC 5280
Db 5340 GTCAATGGAAGAAACCAACCAAGGTCCAAAGCGAGCAAGAGATCCAGAGACAGAAAGATC 5399
Qy 5281 TFCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCAAACATGCCACAGATCAACTG 5340
Db 5400 TFCAGGGGCTAGAAATCTGTTGCTATGGGCCCTTCCAAACATGCCACAGATCAACTG 5459
Qy 5341 GAAATGATGCTACAGCTGTGTGCTCTTCTGTGTGAGAGGCTTTCATCATTCACCTT 5400
Db 5460 GAAATGATGCTACAGCTGTGTGCTCTTCTGTGTGAGAGGCTTTCATCATTCACCTT 5519
Qy 5401 GGCACAGGTGTCCACCCCAATTTGTGTGTGTGAGCAGATGCTGACAGAGCAATGAC 5460
Db 5520 GGCACAGGTGTCCACCCCAATTTGTGTGTGTGAGCAGATGCTGACAGAGCAATGAC 5579
Qy 5461 TTCATGCAATTTGGGCAAGATGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGAC 5520
Db 5580 TTCATGCAATTTGGGCAAGATGTGAGGCACTGTGTGTGACCCGAGAGTGGGTGTGAC 5639
Qy 5521 AGTGTAGCACTCTACAGTGCAGGAGCTGACACCTACCTGATACCCAGATCCCCAC 5580
Db 5640 AGTGTAGCACTCTACAGTGCAGGAGCTGACACCTACCTGATACCCAGATCCCCAC 5699
Qy 5581 AGCCACTAC 5589
Db 5700 AGCCACTAC 5708

RESULT 15

US-08-986-106-1

; Sequence 1, Application US/08986106

; Patent No. 6177410

; GENERAL INFORMATION:

; APPLICANT: HOLT, JEFFREY T.

; APPLICANT: JENSEN, ROY A.

; APPLICANT: KING, MARY-CLAIRE

; APPLICANT: STEINER, MITCHELL S.

; APPLICANT: ROBINSON-BENION, CHERYL L.

; APPLICANT: THOMPSON, MARILYN E.

; TITLE OF INVENTION: THERAPEUTIC METHODS FOR

; TITLE OF SEQUENCES: 26

; NUMBER OF SEQUENCES: 26

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: ARLES A. TAYLOR, JR.

; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER

; STREET: BOULEVARD

; CITY: DURHAM

; STATE: NORTH CAROLINA

; COUNTRY: USA

; ZIP: 27707

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage

; COMPUTER: IBM PC/XT/AT compatible

; OPERATING SYSTEM: Windows 3.1

; SOFTWARE: WORD PERFECT 6.1 and ASCII

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/986,106

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/603,753

; FILING DATE: 20 FEB 1996

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INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 5712

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

FEATURES:

NAME/KEY: BRCA1

LOCATION: GenBank accession no. U14680

PUBLICATION INFORMATION:

AUTHORS: Miki, Y., et. al.

TITLE: A strong candidate gene for the breast and

TITLE: ovarian cancer susceptibility gene BRCA1.

JOURNAL: Science

VOLUME: 266

PAGES: 66-71

DATE: 1994

US-08-986-106-1

Query Match 99.8%; Score 5579.4; DB 3; Length 5712;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 5583; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Search completed: June 12, 2004, 08:37:17
Job time : 34% secs

GenCore version 5.1.6
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CM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 13:13:20 ; Search time 20923 Seconds
(without alignments)
11577.891 Million cell updates/sec

Title: US-09-734-672a-3_COPY_120_5708
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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1: gb.ba.*

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41: em.htgo.other.*

pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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3	5587.4	100.0	5711	6	AR007333	AR007333 Sequence
4	5587.4	100.0	5711	6	AR112808	AR112808 Sequence
5	5587.4	100.0	5711	6	IS9546	IS9546 Sequence 1
6	5581	99.9	5711	6	AR007334	AR007334 Sequence
7	5581	99.9	5711	6	AR112810	AR112810 Sequence
8	5579.4	99.8	5711	6	AR033056	AR033056 Sequence
9	5579.4	99.8	5711	6	AX659576	AX659576 Sequence
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32	5567.4	99.6	5710	6	I40797	I40797 Sequence 6
33	5567.4	99.6	5710	6	AR278114	AR278114 Sequence
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36	5565.4	99.6	5709	6	AR048664	AR048664 Sequence
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38	5565.4	99.6	5709	6	I40793	I40793 Sequence 2
39	5565.4	99.6	5709	6	I40798	I40798 Sequence 7
40	5565.4	99.6	5709	6	I40799	I40799 Sequence 8
41	5565.4	99.6	5709	6	I40800	I40800 Sequence 9
42	5565.4	99.6	5709	6	AR278110	AR278110 Sequence
43	5565.4	99.6	5709	6	AR278115	AR278115 Sequence
44	5565.4	99.6	5709	6	AR278116	AR278116 Sequence
45	5565.4	99.6	5709	6	AR278117	AR278117 Sequence

ALIGNMENTS

RESULT 1	AR007335	Sequence 5 from patent US 5750400.	5711 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	AR007335	Sequence 5 from patent US 5750400.	5711 bp	DNA	linear	PAT 04-DEC-1998
DEFINITION	AR007335	Sequence 5 from patent US 5750400.	5711 bp	DNA	linear	PAT 04-DEC-1998
ACCESSION	AR007335	Sequence 5 from patent US 5750400.	5711 bp	DNA	linear	PAT 04-DEC-1998
VERSION	AR007335.1	GI:9966819	5711 bp	DNA	linear	PAT 04-DEC-1998
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unknown.					
REFERENCE	1 (bases 1 to 5711)					
AUTHORS	Murphy,P.D., Allen,A.C., Alvares,C.P., Critz,B.S., Olson,S.J., Schelter,D.B. and Zeng,B.					
TITLE	Coding sequences of the human BRCA1 gene					
JOURNAL	Patent: US 5750400-A 5 12-MAY-1998;					

FEATURES		Location/Qualifiers	
source		1..5711	
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		/mol_type="unassigned DNA"	
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Query Match 100.0%; Score 5589; DB 6; Length 5711;			
Best Local Similarity 100.0%; Pred. No. 0;			
Matches 5589; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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DB	120	ATGGAATTATCTGCTCTTCGGGTTGAAGAGTACAAATGTCTTAATGTCTATGCAAAA	179
QY	61	ATCTTAGAGTCCCATCTGCTCGAGTGTGATCAAGAACCTGTCTCCAAAGTGTGAC	120
DB	180	ATCTTAGAGTCCCATCTGCTCGAGTGTGATCAAGAACCTGTCTCCAAAGTGTGAC	239
QY	121	CACATATTTTGCAAATTTTGGATGCTGAACTTCTCAACAGAGAAAGGGCCCTTCACAG	180
DB	240	CACATATTTTGCAAATTTTGGATGCTGAACTTCTCAACAGAGAAAGGGCCCTTCACAG	299
QY	181	TGTCCTTTATGTAAGATGATATTAACCAAAAGAGGCTTACAGAAAGTACAGATTAGT	240
DB	300	TGTCCTTTATGTAAGATGATATTAACCAAAAGAGGCTTACAGAAAGTACAGATTAGT	359
QY	241	CAACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTTCAGCTTGACACAGGTTTGGAG	300
DB	360	CAACTTGTGAAGAGCTATTGAAATCATTTGTGCTTTTCAGCTTGACACAGGTTTGGAG	419
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DB	420	TATGCAAAACAGCTATAATTTTGCAAAAGAGAAATAACTCTCTCGAACATCTAAAGAT	479
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DB	540	GAACCCGAAATCTCTCTGAGAGATACCGTTAATAGGCAACTTCTAACTTGGGA	599
QY	481	ACTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTTCAAGAGAGCTGTCTACATT	540
DB	600	ACTGTGAGAACTCTGAGGACAAAGCAGGAGTACAACTTCAAGAGAGCTGTCTACATT	659
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DB	660	GAATTTGGGATCTGATTTCTTGAGAGATACCGTTAATAGGCAACTTATTCAGTGTGGGA	719
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DB	720	GATCAAGAAATTTGTTACAAATCACCCCTCAAGGAAACGAGGATGAATTCAGTTGGATTCT	779
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DB	780	GCAAAAAGGCTGCTGTGAAATTTCTGAGACGAGTGTAAACAAATCTGAACATCATCAA	839
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DB	840	CCCAAGTAATAATGATTTGAACAACAATGAGAGCGTGCAGTGAAGGCAATCCAGAAAG	899
QY	781	TATCAGGGTAGTCTGTTTCAAACTTGATGTGAGAGCCATGTGGCACAATATCTCATGCC	840
DB	900	TATCAGGGTAGTCTGTTTCAAACTTGATGTGAGAGCCATGTGGCACAATATCTCATGCC	959
QY	841	AGCTCATATACAGATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAATGATAGAA	900
DB	960	AGCTCATATACAGATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAATGATAGAA	1019
QY	901	AAGGCTGAATTTCTTAATAAAGCAACAGCCTGGCTTACAGAGGCCCAACATACAGA	960
DB	1020	AAGGCTGAATTTCTTAATAAAGCAACAGCCTGGCTTACAGAGGCCCAACATACAGA	1079

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Db	2160	AGTAAAGCCAAATGAAACAGACAGTAAAGAAAGACATGACAGTGAATCTTTCCCGAGAGCTG	2219
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Qy	2281	GAAGAATCTGTAGAGAGPAGCAGTATTTCACTCGTACTCGTACTGTAATTATGGCACTCAG	2340
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Qy	2341	GAAAGTATCTCGTTACTGGAGTTTAGCACCTCTAGGGAGGCCAAAGACAGAACCAATAAA	2400
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Db	2520	TGTTGTAGTCAGTGTGCAGCATTTTCAAAAACCCCAAGGCACTAAATTCATGCTGTGTCTCCAA	2579
Qy	2461	GATTAATAGAAATGACACAGAAAGCCTTTAAGTATCCATTTGGGACATGAAGTTAACCAAGT	2520
Db	2580	GATTAATAGAAATGACACAGAAAGCCTTTAAGTATCCATTTGGGACATGAAGTTAACCAAGT	2639
Qy	2521	CGGAAACCAAGCATAGAAATGGAAAGAGTGAACCTGATGCTCAGTATTTTGCAGAAATACA	2580
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Db	2700	TTCAAGGTTTCAAAGCGCCAGTCAATTTGCTCTGTTTTCAAATCCAGAAAATGCAGAAAG	2759
Qy	2641	GAATGTGCAACATTTCTCTGCCCATCTCTGGGTCCTTAAAGAAACAAAGTCCAAAGTCACT	2700
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Db	2940	AATGCCAAATGTAGTATCAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGC	2999
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Qy	3001	GAAAACTTTGAGAACATTCATGTCCAACTCGAAAGAAATGGGAAATGAGAACATTCACA	3060
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Qy	3061	AGTACAGTGAACAAATTTAGCCCTTAATACATTTAGAGAAAATGTTTTTAAAGAGGCCAGC	3120
Db	3180	AGTACAGTGAACAAATTTAGCCCTTAATACATTTAGAGAAAATGTTTTTAAAGAGGCCAGC	3239
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Qy	2701	TTTGAATGTGAACAAAGGAAG	AAATTCAGGAAAGAAATGAGTCT	TAATATCAAGCCCTGTA	2760	
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Qy 1621 CAGAACTGCTCAAGTGAATGATTAATTAATAGTGTCTATCAGAGTAAACAAAGGTGAT 1680
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Qy 1681 TCTATTGAGAAATGAGAAAAATCTTAACCCAAATGAAATCACTCGAAAAAGAAATCTGCTTTC 1740
Db 1800 TCTATTGAGAAATGAGAAAAATCTTAACCCAAATGAAATCACTCGAAAAAGAAATCTGCTTTC 1859
Qy 1741 AAAAGAAAGCTGAACCTATAGCAGCAGTATAGCAATATAGCAATGGAATCTGAAATTAATATC 1800
Db 1860 AAAAGAAAGCTGAACCTATAGCAGCAGTATAGCAATATAGCAATGGAATCTGAAATTAATATC 1919
Qy 1801 CACAATTCAAAGACACCTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCATATT 1860
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Db 1980 CATGCGCTTGAATAGTGTAGTGAATCTAAGCCCACTAATTTGTACTGAAATTTGCAA 2039
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Db 2040 ATTGATAGTTGTTCTAGCAGTGAAGATAGGCTGAGGAGGAAGTCTTCTACAGGCATATT 2099
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DB |||||
QY 3660 GTCCAGAGAGGAGCTTACGAGAGGCTTACGCTTACCCATACACATTTGGCTCAG 3719
DB |||||
QY 3601 GGTTCACGAGAGGGCCAAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAAGAT 3660
DB |||||
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LOCUS
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ACCESSION AR112808
VERSION AR112808.1 GI:14092708
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.

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1 (bases 1 to 5711)
Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,
Thompson, B., and Zeng, B.
Coding sequences of the human BRCA1 gene
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Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 5587.4; DB 6; Length 5711;
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Matches 5588; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy	4501	TGCCCATCATTAGATAGTGGTGAATGCAAGTTGCTCTGGAGTCTTCAGAAATAGA	4560
Db	4620	TGCCCATCATTAGATAGTGGTGAATGCAAGTTGCTCTGGAGTCTTCAGAAATAGA	4679
Qy	4561	AATTACCCATCTCAAGAGGAGCTCATTAAGTGTGTCATGTGAGGAGGAGCAACAGCTGGAA	4620
Db	4680	AATTACCCATCTCAAGAGGAGCTCATTAAGTGTGTCATGTGAGGAGGAGCAACAGCTGGAA	4739
Qy	4621	GAGTCTGGGCCACAGATTTGAAGGAAACATCTTACTTGCACAGGCAAGATCTAGAGGGA	4680
Db	4740	GAGTCTGGGCCACAGATTTGAAGGAAACATCTTACTTGCACAGGCAAGATCTAGAGGGA	4799
Qy	4681	ACCCCTTACCTGGAACTCGAAATCAGCCTCTTCTGATGACCACTGAAATCTGATCTCTCT	4740
Db	4800	ACCCCTTACCTGGAACTCGAAATCAGCCTCTTCTGATGACCACTGAAATCTGATCTCTCT	4859
Qy	4741	GAAGACAGAGCCCCAGAGTCAGTCTGTTTGGCAACATACATCTTCAACCTCTGCATTCG	4800

DB	4860	GAAGACAGAGCCCGAGAGTCAGCTCGTGTGGTGGCAACATCCTCTCAAGCCTCTGCATTG	4919
QY	4801	AAAGTCTCCCAAATTGAAAGTTGCAGAAATCTGCCCAGGGTCCAGCTGCTGCTCATCTACT	4860
DB	4920	AAAGTCTCCCAAATTGAAAGTTGCAGAAATCTGCCCAGGGTCCAGCTGCTGCTCATCTACT	4979
QY	4861	GATACTCTCGGTATTAATGCAATGGAAGAAGTGTGAGGAGGAGAGCCAGAAATTCACA	4920
DB	4980	GATACTCTCGGTATTAATGCAATGGAAGAAGTGTGAGGAGGAGAGCCAGAAATTCACA	5039
QY	4921	GCTTCAACAGAAAGGGTCAACAAAAGAAATGTCATGTTGTTGTTCTGSCCTGCAGCCCGAGAA	4980
DB	5040	GCTTCAACAGAAAGGGTCAACAAAAGAAATGTCATGTTGTTGTTCTGSCCTGCAGCCCGAGAA	5099
QY	4981	GAATTTATGCTCGGTATTAATGCAATGGAAGAAGTGTGAGGAGGAGAGCCAGAAATTCACA	5040
DB	5100	GAATTTATGCTCGGTATTAATGCAATGGAAGAAGTGTGAGGAGGAGAGCCAGAAATTCACA	5159
QY	5041	ACTGAAGAGACTACTCATATGTTGTTATGAAACAGATGCTGAGTTGTGTGTGAACCGGACA	5100
DB	5160	ACTGAAGAGACTACTCATATGTTGTTATGAAACAGATGCTGAGTTGTGTGTGAACCGGACA	5219
QY	5101	CTGAATTAATTTCTAGGAATTCGGGAGGAGAAATGGTAGTTAGCTATTTCCTGGGTGACC	5160
DB	5220	CTGAATTAATTTCTAGGAATTCGGGAGGAGAAATGGTAGTTAGCTATTTCCTGGGTGACC	5279
QY	5161	CAGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTCAAGGTCAAGAGAGATGTG	5220
DB	5280	CAGTCTATTAAAGAAAGAAAAATGCTGAATGAGCATGATTTTCAAGGTCAAGAGAGATGTG	5339
QY	5221	GTCAATGGAGAAACCCACCAAGTCCAAAGCGAGCAAGAGAAATCCAGAGACAGAAAGATC	5280
DB	5340	GTCAATGGAGAAACCCACCAAGTCCAAAGCGAGCAAGAGAAATCCAGAGACAGAAAGATC	5399
QY	5281	TTCAAGGGGCTAGAAATCTGTGCTATGCGGCCCTTCCACCAATGCCCACAGATCAACTCG	5340
DB	5400	TTCAAGGGGCTAGAAATCTGTGCTATGCGGCCCTTCCACCAATGCCCACAGATCAACTCG	5459
QY	5341	GAATGGATGTGACAGCTGTGTGTGCTTCTGTGTTGAAGGAGCTTTCATCATCAACCTT	5400
DB	5460	GAATGGATGTGACAGCTGTGTGTGCTTCTGTGTTGAAGGAGCTTTCATCATCAACCTT	5519
QY	5401	GGCACAGTGTCCACCCCAATTTGTTGTGTGACCCAGATGCTCGGACAGAGGACAAATGGC	5460
DB	5520	GGCACAGTGTCCACCCCAATTTGTTGTGTGTGACCCAGATGCTCGGACAGAGGACAAATGGC	5579
QY	5461	TTCCATGCAATTTGGGCAGATGTGTAGGCACTCTGTGTTGACCCGAGAGTGGGTGTTGGAC	5520
DB	5580	TTCCATGCAATTTGGGCAGATGTGTAGGCACTCTGTGTTGACCCGAGAGTGGGTGTTGGAC	5639
QY	5521	AGTGTAGCACTTACAGTGCAGAGGAGCTGGACACCTTACTGTATACCCAGATGCCCCAC	5580
DB	5640	AGTGTAGCACTTACAGTGCAGAGGAGCTGGACACCTTACTGTATACCCAGATGCCCCAC	5699
QY	5581	AGCCACTAC 5589	
DB	5700	AGCCACTAC 5708	

RESULT 5

LOCUS	IS9546	5711 bp	DNA	linear	PAT 07-OCT-1997
DEFINITION	Sequence 1 from patent US 5654155.				
ACCESSION	IS9546				
VERSION	IS9546.1	GI:2478178			
KEYWORDS	.				
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J., Scheffer, D.B. and Zeng, B.				

TITLE		Consensus sequence of the human BRCA1 gene	
JOURNAL		Patent: US 5654155-A 1 05-AUG-1997;	
FEATURES	Location/Qualifiers		
	1..5711		
source	organism="unknown"		
	/mol_type="unassigned DNA"		
ORIGIN			
Query Match		100.0%; Score 5587.4; DB 6; Length 5711;	
Best Local Similarity		100.0%; Pred. No. 0;	
Matches 5588; Conservative		0; Mismatches 1; Indels 0; Gaps 0;	
QY	1	ATGGATTATCTGCTCTCCGCTTCAAGAGTACAAATATGTCATATGCTATGCGAGAA	60
DB	120	ATGGATTATCTGCTCTCCGCTTCAAGAGTACAAATATGTCATATGCTATGCGAGAA	179
QY	61	ATCTTAGAGTCCCATCTGCTGAGGTGATCAAGGAACCTGTCTCCACAAAGTGTGAC	120
DB	180	ATCTTAGAGTCCCATCTGCTGAGGTGATCAAGGAACCTGTCTCCACAAAGTGTGAC	239
QY	121	CACATATTTTGCAAAATTTTGCATGCTGAACTTCTCAACGAGAGAAAGGGCCCTTCACAG	180
DB	240	CACATATTTTGCAAAATTTTGCATGCTGAACTTCTCAACGAGAGAAAGGGCCCTTCACAG	299
QY	181	TGTCCTTTATGTAAGATGATATACCAAAAGAGCCCTACAGAAAGTACGAGATTAGT	240
DB	300	TGTCCTTTATGTAAGATGATATACCAAAAGAGCCCTACAGAAAGTACGAGATTAGT	359
QY	241	CAACTCTGTGAAGAGCTATTGAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTGGAG	300
DB	360	CAACTCTGTGAAGAGCTATTGAAATCATTTTGTGCTTTTTCAGCTTGACACAGGTTGGAG	419
QY	301	TATGCAAAAGCTATATTTTGCAAAAAGAGAAATAAATCTCTCTGAAACATCTTAAAGAT	360
DB	420	TATGCAAAAGCTATATTTTGCAAAAAGAGAAATAAATCTCTCTGAAACATCTTAAAGAT	479
QY	361	GAAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGT	420
DB	480	GAAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGT	539
QY	421	GAACCCGAAATTCCTTCCTTGCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTTGGA	480
DB	540	GAACCCGAAATTCCTTCCTTGCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTTGGA	599
QY	481	ACTGTGAGAACTCTGAGACAAAGCAGCGGATCAACCTCAAAAGAGCTGTCTGCTACATT	540
DB	600	ACTGTGAGAACTCTGAGACAAAGCAGCGGATCAACCTCAAAAGAGCTGTCTGCTACATT	659
QY	541	GAATTGGGATCTGATTCTTCTGAAGATACCGTTTAAATAGGCAACTTATTTCAGTGTGGGA	600
DB	660	GAATTGGGATCTGATTCTTCTGAAGATACCGTTTAAATAGGCAACTTATTTCAGTGTGGGA	719
QY	601	GATCAAGAAATGTTACAAATCACCCCTCAAGCAACCGGATGAAATCAGTTTGGATTCT	660
DB	720	GATCAAGAAATGTTACAAATCACCCCTCAAGCAACCGGATGAAATCAGTTTGGATTCT	779
QY	661	GCAAAAAGGCTGTCTGTAATTTTCTGAGAGCGGATGTAAACAAATATCTGAACATCATCAA	720
DB	780	GCAAAAAGGCTGTCTGTAATTTTCTGAGAGCGGATGTAAACAAATATCTGAACATCATCAA	839
QY	721	CCAGTAATATGATTTTGAACACCACTGTGAGAGCGTCCAGCTGAGAGGCATCCAGAAAG	780
DB	840	CCAGTAATATGATTTTGAACACCACTGTGAGAGCGTCCAGCTGAGAGGCATCCAGAAAG	899
QY	781	TATCAGGCTAGTTCTGTTTCAAACTTCATGTGAGCGCATGTGCGACAAATFACTCTATGCC	840
DB	900	TATCAGGCTAGTTCTGTTTCAAACTTCATGTGAGCGCATGTGCGACAAATFACTCTATGCC	959
QY	841	AGCTCATTACAGCATGAGAAACAGCAGTTTATTACTCTAAAGACAGAAATGATAGAA	900
DB	960	AGCTCATTACAGCATGAGAAACAGCAGTTTATTACTCTAAAGACAGAAATGATAGAA	1019
QY	901	AAGGCTGAATTTCTGTAATAAAGCAACACGCTGGCTTAGCAGAGGAGCCAAACATACAGA	960

Db 2100 AGGCACAGCAGAAACCTTACAACTCATGGAAGGTAAAGAACTTGCACTGGAGCCAGAG 2159
Qy 2041 AGTAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTGTACTTTCCCAAGAGCTG 2100
Db 2160 AGTAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTGTACTTTCCCAAGAGCTG 2219
Qy 2101 AAGTTAAACAATGACACCTGGTTCTTTTACTAAGTGTTCATATACCACTGACCTAAAGAA 2160
Db 2220 AAGTTAAACAATGACACCTGGTTCTTTTACTAAGTGTTCATATACCACTGACCTAAAGAA 2279
Qy 2161 TTTGTCAATCTAGCTTTCCAGAGAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTG 2220
Db 2280 TTTGTCAATCTAGCTTTCCAGAGAGAGAAAGAAAGAGAACTAGAAACAGTTTAAAGTG 2339
Qy 2221 TCTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCAAACT 2280
Db 2340 TCTAATATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCAAACT 2399
Qy 2281 GAAAGATCTGAGAGAGTACAGATATTTCACTGGTACTCTGATATGACCTCAG 2340
Db 2400 GAAAGATCTGAGAGAGTACAGATATTTCACTGGTACTCTGATATGACCTCAG 2459
Qy 2341 GAAAGATCTGTTACTGGAAGTATGACACTCTAGGAGAGGCAAAAACAGAAACCAATAAA 2400
Db 2460 GAAAGATCTGTTACTGGAAGTATGACACTCTAGGAGAGGCAAAAACAGAAACCAATAAA 2519
Qy 2401 TGTGTGAGTCAAGTGTGACAGATTTGAAACCCCAAGGAGCTAACTCATGGTGTGTTCCAAA 2460
Db 2520 TGTGTGAGTCAAGTGTGACAGATTTGAAACCCCAAGGAGCTAACTCATGGTGTGTTCCAAA 2579
Qy 2461 GATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTTAAACACAGT 2520
Db 2580 GATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTTAAACACAGT 2639
Qy 2521 CGGGAACCAAGCTAGAAATGGAAGAGTGAAGTGAAGTCTGATGCTCAGTATTTCCAGATACA 2580
Db 2640 CGGGAACCAAGCTAGAAATGGAAGAGTGAAGTGAAGTCTGATGCTCAGTATTTCCAGATACA 2699
Qy 2581 TTCAAGGTTTCAAAGCGCCAGTCATTGCTCTGTTTCAAATCCAGGAAATGCGAGAAGAG 2640
Db 2700 TTCAAGGTTTCAAAGCGCCAGTCATTGCTCTGTTTCAAATCCAGGAAATGCGAGAAGAG 2759
Qy 2641 GAATGTGCAACTTCTGCCCCA CTCTGGTCTCTTAAGAAACAAAGTCCCAAGTCACT 2700
Db 2760 GAATGTGCAACTTCTGCCCCA CTCTGGTCTCTTAAGAAACAAAGTCCCAAGTCACT 2819
Qy 2701 TTTGAAATGCAACAAAGAGAAATCAAGAAAGATGAGTCTTAATCAAGCTCTGTA 2760
Db 2820 TTTGAAATGCAACAAAGAGAAATCAAGAAAGATGAGTCTTAATCAAGCTCTGTA 2879
Qy 2761 CAGACAGTTAATCACTGACGGCTTCTCTGTTGGTTCAGAAAGATGAAAGCCAGTTGAT 2820
Db 2880 CAGACAGTTAATCACTGACGGCTTCTCTGTTGGTTCAGAAAGATGAAAGCCAGTTGAT 2939
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Db 2940 AATGCCAATGATGATCAAGAGGCTCTAGTCTTCTATCATCTCAGTTCAGAGGC 2999
Qy 2881 AACGAACTGGACTCACTTCACTCCAAATAAACATGCACTTTTACAAACCCCATATCGTATA 2940
Db 3000 AACGAACTGGACTCACTTCACTCCAAATAAACATGCACTTTTACAAACCCCATATCGTATA 3059
Qy 2941 CCACCACTTTTCCCACTCAAGTCATTGTTAAACCTTAAGTGAAGAAATCTGCTAGAG 3000
Db 3060 CCACCACTTTTCCCACTCAAGTCATTGTTAAACCTTAAGTGAAGAAATCTGCTAGAG 3119
Qy 3001 GAAACCTTTGAGGAACATTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACATTTCCA 3060
Db 3120 GAAACCTTTGAGGAACATTCAATGTCACTGAAAGAGAAATGGGAAATGAGAACATTTCCA 3179
Qy 3061 AGTACAGTACACATTTAGCCGTATTAACATTAGAGAAATGTTTTTAAAGGAGCCAGC 3120
Db 3180 AGTACAGTACACATTTAGCCGTATTAACATTAGAGAAATGTTTTTAAAGGAGCCAGC 3239

Qy 3121 TCAAGCAATTAATGAAGTAGTTCACGTACTAATGAAGTGGGCTCCAGTATTAAATGAA 3180
Db 3240 TCAAGCAATTAATGAAGTAGTTCACGTACTAATGAAGTGGGCTCCAGTATTAAATGAA 3299
Qy 3181 ATAGGTTTCAGTGTAGTCAAAACATTTCAAGCAGAACATAGGTAGAGAAACAGAGGGCCAAAATTG 3240
Db 3300 ATAGGTTTCAGTGTAGTCAAAACATTTCAAGCAGAACATAGGTAGAGAAACAGAGGGCCAAAATTG 3359
Qy 3241 AATGCTATCTGTAGATTAGGGTTTTGGCAA CCGTAGGCTCTATAAAACAAGCTCTTCTCTGGA 3300
Db 3360 AATGCTATCTGTAGATTAGGGTTTTGGCAA CCGTAGGCTCTATAAAACAAGCTCTTCTCTGGA 3419
Qy 3301 AGTAATTTGTAAGCATCTGAAATATAAAAGCAAGATATGAAGAGCTAGTTCAGACTGTT 3360
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Qy 3361 AATACAGATTTCTCTCATATCTGATTTTCAATATACTTGAAGACAGCTTATGGGAAGTAGT 3420
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Qy 3421 CATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATCGTGAATAAAG 3480
Db 3540 CATGCATCTCAGGTTTGTCTGAGACACCTGATGACCTGTTAGATGATCGTGAATAAAG 3599
Qy 3481 GAAGATATACTAGTTTCTGANAATGACATTAAGGAAAGTTCTGCTGTTTTTACAAAAGC 3540
Db 3600 GAAGATATACTAGTTTCTGANAATGACATTAAGGAAAGTTCTGCTGTTTTTACAAAAGC 3659
Qy 3541 GTCCAGAGAGGAGCTTACGAGGACTCTAGGCCCTTACCCATACACATTTGGGCTCAG 3600
Db 3660 GTCCAGAGAGGAGCTTACGAGGACTCTAGGCCCTTACCCATACACATTTGGGCTCAG 3719
Qy 3601 GGTTCACGAAGAGGGCCAAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGAAGAT 3660
Db 3720 GGTTCACGAAGAGGGCCAAAGAAATTAGAGTCTCTCAGAAGAGAACTTATCTAGTGAAGAT 3779
Qy 3661 GAAGAGTTTCCCTGCTTCCAACTCTGTTTATTTGGTAAAGTAAACATATACCTTCTCAG 3720
Db 3780 GAAGAGTTTCCCTGCTTCCAACTCTGTTTATTTGGTAAAGTAAACATATACCTTCTCAG 3839
Qy 3721 TCTACTAGGATAGCAGCGTTGCTGACCGAGTGTCTGCTAAGAAACACAGAGGAGAAATTTA 3780
Db 3840 TCTACTAGGATAGCAGCGTTGCTGACCGAGTGTCTGCTAAGAAACACAGAGGAGAAATTTA 3899
Qy 3781 TTATCATTTGAAGATAGCTTAAATGATGTCAGTAAACAGGTAATA TTGGCAAGGCACTCT 3840
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Qy 3841 CAGGACATCACCTTAGTGGAGAAACAAATGTTCTGCTAGCTTGTGTTTCTTCCAGAGTGC 3900
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Qy 3901 AGTGAATTTGAAGACTTGAAGTCAAAATACAAA CACCCAGGATCCTTTCTGATTTGTTCT 3960
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Qy 4021 GTTTCAGATCATCAAGAAAGAGGAAACCGGCTTCGAAAGAAATTAATCAAGAGAGCAAGC 4080
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Qy 4081 ATGATTTCAAACCTTAGGTAAGCAGCATCTGGGTGTGAGAGTGAAGCAAGGCTCTCTGAA 4140
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Qy 4141 GACTGCTCAGGCTATCTCTCAGAGTGAATTTAAACCACTCAGCAGAGGAGTACCATG 4200
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DB 480 GAAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACATCTCTACAGAT 539
QY 421 GAACCCGAAATCCTTCCTCCAGGAAACAGTCTCAGTGTCCAACTCTCTAACTTGEA 480
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QY 481 ACTGTGAACTCTGAGGACAAAGCAGCGGATACACCTCAAAAGAGCTGTCTACAT 540
DB 600 ACTGTGAACTCTGAGGACAAAGCAGCGGATACACCTCAAAAGAGCTGTCTACAT 659
QY 541 GAATTTGGGATCTGATCTTCTGAGATACCGTAAATAGGCAACTTATGCGGTGGGA 600
DB 660 GAATTTGGGATCTGATCTTCTGAGATACCGTAAATAGGCAACTTATGCGGTGGGA 719
QY 601 GATCAAGAAATGTTTACAAATCACCCCTCAAGGAAACCGGATGAAATCAGTTTGGATCT 660
DB 720 GATCAAGAAATGTTTACAAATCACCCCTCAAGGAAACCGGATGAAATCAGTTTGGATCT 779
QY 661 GCACAAAGGCTGCTTGTGAATTTCTGAGACGGATGTAAACAAATACATCAATCA 720
DB 780 GCACAAAGGCTGCTTGTGAATTTCTGAGACGGATGTAAACAAATACATCAATCA 839
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DB 840 CCCAGTAATATGATTTGAACACCACTGAGAGCGGTGCAGCTGAGAGGCATCCAGAAAG 899
QY 781 TATCAGGGTATGCTGTTTCAAACTGTCATGTGAGCGCATGTGGCACAATATCTATGCC 840
DB 900 TATCAGGGTATGCTGTTTCAAACTGTCATGTGAGCGCATGTGGCACAATATCTATGCC 959
QY 841 AGCTCATTTACAGCATGAGAACAGCAGTGTATTTACTTCACTAAAGACAGAAATGTAGAA 900
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QY 1141 AAAGTTAATGATGCTTTTCCAGAAAGTATGAACTGTTAGTGTCTGATGACTCACATGAT 1200
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QY 1741 AAAACGAAAGCTGAACCTTATAGCAGCAGTATTAAGCAATATGGAATCTCGAAATTTAAATATC 1800
DB 1860 AAAACGAAAGCTGAACCTTATAGCAGCAGTATTAAGCAATATGGAATCTCGAAATTTAAATATC 1919
QY 1801 CACAAATTTCAAAAGCAGCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCAATTT 1860
DB 1920 CACAAATTTCAAAAGCAGCTTAAAGAAATAGGCTGAGGAGGAAGTCTTCTACAGGCAATTT 1979
QY 1861 CATGCGCTTGAACCTAGTGTAGTAAATCTTAAGCCCACTTAATTTGTACTGAAATTCGAA 1920
DB 2039 CATGCGCTTGAACCTAGTGTAGTAAATCTTAAGCCCACTTAATTTGTACTGAAATTCGAA 2039
QY 1921 ATTGTAGTGTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATTTGCCAGTC 1980
DB 2040 ATTGTAGTGTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATTTGCCAGTC 2099
QY 1981 AGCCACAGCGGAAACCTCAACCTCTGAGAGTAAAGAACTCTCACTGCGGCGGCAAG 2040
DB 2100 AGCCACAGCGGAAACCTCAACCTCTGAGAGTAAAGAACTCTCACTGCGGCGGCAAG 2159
QY 2041 AGTAAACAAGCCAAATGAAACAGACCAAGTAAAGAACTAGCATGATATCTTTCCAGAGCTG 2100
DB 2160 AGTAAACAAGCCAAATGAAACAGACCAAGTAAAGAACTAGCATGATATCTTTCCAGAGCTG 2219
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DB 2220 AGTTTAAACAATGCACTGCTGTTCTTTTCTAAGTGTCTAATACCACTGAACTTAAAGAA 2279
QY 2161 TTTGTCAATCTCTAGCTTCCCAAGAGAAAGAAAGAGAGAACTAGAAACAGTTAAAGTG 2220
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DB 2400 GAAAGATCTGTAGAGAGTACGATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2459
QY 2341 GAAAGATCTGTGTTACTGGAAGTTAGCACTCTAGGGAAGCGCAAAAACAGAACCAATAA 2400
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QY 2521 CGGGAAACAGGCAATGAAATGGAAGAAAGTGAATCTTGTGCTGCTGCTGCTGCTGCTGCTGCTG 2580

Db 2640 CGGAAACAAACATAGAAATGGAAGAAAGTGAACCTTGATGCTCAGTATTTGCGAATACA 2699
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Db 2700 TTCAAGGTTTCAAAAGCCGAGTCATTTGCTCTGTTTCAAAATCCAGGAATGCAAGAGAG 2759
Qy 2641 GAATGTCGAACATTTCTCTGCCACTCTGGGTCCTTTAAAGAAAACAAAGTCCAAAAGTCACT 2700
Db 2760 GAATGTCGAACATTTCTCTGCCACTCTGGGTCCTTTAAAGAAAACAAAGTCCAAAAGTCACT 2819
Qy 2701 TTTGAATGTGAACAAAAGGAGAAATCAAGGAAGAAATGAGTCTTAATATCAAGCCCTGTA 2760
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[illegible]

Thurber, D. and Zeng, B.
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 Location/Qualifiers
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ORIGIN

Query Match 99.9%; Score 5581; DB 6; Length 5711;
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Qy 121 CACATATTTTGC AAAATTTTGCATGCTGGAACCTTCTCAACCCAGAAAGAGGCGCTTCCAG 180
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Qy 181 TGTCTTTATGTAAGATGATATATACCAAAGAGGCTACAGAAAGTACGAGATTTAGT 240
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VERSION AR033056.1 GI:5948661
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Yeung,A.T.
TITLE Mismatch endonuclease and its use in identifying mutations in
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JOURNAL Patent: US 5869245-A 1 09-FEB-1999;
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REFERENCE 1
AUTHORS dalla Venezia,N., Megnard,C., Lenoir,G. and Sinilnikova-Brard,O.
TITLE Brcal/acc alpha molecular complexes, diagnostic and therapeutic applications
JOURNAL Patent: WO 0210897-A 15 19-DEC-2002;
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RESULT 10

HSU14680

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLES

JOURNAL

FEATURES

source

gene

HSU14680 5711 bp mRNA linear PRI 10-JUN-2002
Homo sapiens breast and ovarian cancer susceptibility (BRCA1) mRNA,
complete cds.

UI4680

UI4680.1 GI:555931

Homo sapiens (human)

Homo sapiens

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1 (bases 1 to 5711)

Miki, Y., Svendsen, J., Shattuck-Eidens, D., Futreal, P.A., Harshman, K.,

Tavtigian, S., Liu, Q., Cochran, C., Bennett, L.M., Ding, W., Bell, R.,

Rosenthal, J., Huseby, C., Tran, T., McClure, M., Frye, C., Hattier, T.,

Phelps, R., Haugen-Strano, A., Katcher, H., Yakumo, K., Gholami, Z.,

Shaffer, D., Stone, S., Bayer, S., Wray, C., Bogden, R., Dayananth, P.,

Ward, J., Tonin, P., Narod, S., Bristow, P.K., Norris, F.H.,

Helvering, L., Morrison, P., Rostock, P., Lai, M., Barrett, J.C.,

Lewis, C., Neuhausen, S., Cannon-Albright, L., Goldgar, D., Wiseman, R.,

Kamb, A. and Skolnick, M.H.

A strong candidate for the breast and ovarian cancer susceptibility

gene BRCA1

Science 266 (5182), 66-71 (1994)

95025896

7545954

2 (bases 1 to 5711)

Skolnick, M.H.

Direct Submission

Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and

the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City,

UT 84108, USA

Location/Qualifiers

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RESULT 12
ARL18507
LOCUS      ARL18507
DEFINITION Sequence 1 from patent US 6149903.
ACCESSION ARL18507
VERSION   ARL18507.1 GI:14100417
KEYWORDS  Unknown.
SOURCE    Unknown.
ORGANISM  Unclassified.
REFERENCE 1 (bases 1 to 5712)
AUTHORS   Holt,J.T., Jensen,R.A., King,M.-C., Page,D.L., Szabo,C.I.,
           Jetton,T.L., Robinson-Benion,C.E. and Thompson,M.E.
TITLE      Characterized BRCA1 and BRCA2 proteins and screening and
           therapeutic methods based on characterized BRCA1 and BRCA2 proteins
JOURNAL    Patent: US 6149903-A 1 21-NOV-2000;
FEATURES   location/Qualifiers
           source
           1..5712
           /organism="unknown"
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ORIGIN
Query March 99.8%; Score 5579.4; DB 6; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 0; Gaps 0;
Matches 5583; Conservative 0; Indels 0;

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QY      61 ATCTTAGAGTGCCCATCTGCTGAGTGTATCAAGGACCTGTCTCCACAAAGTGTGAC 120
Db      180 ATCTTAGAGTGCCCATCTGCTGAGTGTATCAAGGACCTGTCTCCACAAAGTGTGAC 239
QY      121 CACATATTTTGCATATTTTGCATGCTGAACTTCTCAACCAAGAAAGGCGCTTTCACAG 180
Db      240 CACATATTTTGCATATTTTGCATGCTGAACTTCTCAACCAAGAAAGGCGCTTTCACAG 299
QY      181 TGTCTTTTATGTAAGATGATATACCAAAAGGAGCCCTACAGAAAGTACAGATTTAGT 240
Db      300 TGTCTTTTATGTAAGATGATATACCAAAAGGAGCCCTACAGAAAGTACAGATTTAGT 359
QY      241 CAACTTGTGTAAGAGCTATTGAAATCATTTTGTGCTTTTCAGCTTGACACAGGTTTGGAG 300
Db      360 CAACTTGTGTAAGAGCTATTGAAATCATTTTGTGCTTTTCAGCTTGACACAGGTTTGGAG 419
QY      301 TATGCAACAGCTATATTTTGCACAAAAGGAAATATCTCTCTGGAACATCTAAAGAT 360
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QY      421 GAAACCCGAAATCTCTCTGTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTTAAACCTTGA 480
Db      540 GAAACCCGAAATCTCTCTGTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTTAAACCTTGA 599
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QY      1201 GGGAGTCTGAATCAAAATGCAAGTAGCTGATGTATTGGACGTTCTTAAATAGGCTAGAT 1260
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QY      1321 ATATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATA 1380
Db      1440 ATATGTAAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATA 1499
QY      1381 TTTGGGAAAACCTATTCGGAAGAGGCGAGGCTCCCGAACTTAAGCCGATGTAACCTGAAAT 1440
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RESULT 13

AR125601
LOCUS 5712 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 1 from patent US 6177410.
ACCESSION AR125601
VERSION AR125601.1 GI:14111663
KEYWORDS Unknown.
SOURCE Unclassified.
ORGANISM 1 (bases 1 to 5712)
REFERENCE Holt, J.T., Jensen, R.A., King, M.-C., Steiner, M.S.,

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5700	Db	AGCCACTAC	5708

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Job time : 20932 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 19:58:38 ; Search time 13193 Seconds
(without alignments)
12926.773 Million cell updates/sec

Title: US-09-734-672A-3

Perfect score: 5711

Sequence: 1 AGCTCGTGAGACTTCCTGG.....TCCGCCACGACCACTACTGA 5711

Scoring table:

IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: em_estba.*
2: em_esthum.*
3: em_estin.*
4: em_estmi.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_hic.*
9: gb_est1.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: em_gss_hum.*
18: em_gss_inv.*
19: em_gss_pln.*
20: em_gss_vrt.*
21: em_gss_fun.*
22: em_gss_mam.*
23: em_gss_mus.*
24: em_gss_pro.*
25: em_gss_rod.*
26: em_gss_phg.*
27: em_gss_vrl.*
28: gb_gss1.*
29: gb_gss2.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2061.4	36.1	2101	11 BC012577	BC012577 Homo sapi
2	2055.6	36.0	2090	11 BC030969	BC030969 Homo sapi
3	1416.4	24.8	1578	11 BC038947	BC038947 Homo sapi
4	968.8	17.0	1919	11 AK086173	AK086173 Mus muscu

5	863	15.1	962	13	BQ068830
6	841.4	14.7	1089	12	BM452288
7	811.8	14.2	845	9	AU122476
8	760.2	13.3	783	9	AU142729
9	750.6	13.1	789	14	CK000353
10	746.4	13.1	933	13	BUI71200
11	738.8	12.9	743	12	BQ681276
12	734.6	12.9	899	13	BQ422380
13	706.2	12.4	878	13	BQ215100
14	701.2	12.3	739	14	CF121736
15	698	12.2	856	13	BUI47444
16	688	12.0	702	9	AU125312
17	687.6	12.0	747	12	BG777447
18	686.6	12.0	739	10	BF508987
19	686.4	12.0	987	12	BM800251
20	686.6	11.5	900	10	BF791668
21	651.6	11.4	938	12	BG257190
22	639	11.2	675	9	AL704228
23	631	11.0	631	14	CB155501
24	617.6	10.8	921	12	BG178466
25	603.8	10.6	630	9	AI992040
26	593	10.4	906	13	BQ878445
27	593	10.4	909	13	BQ676829
28	593	10.4	922	13	BUI94336
29	593	10.4	933	13	BQ683955
30	591.4	10.4	627	9	AI589028
31	591	10.3	724	9	AI915085
32	591	10.3	800	10	BF794879
33	586	10.3	947	13	BQ679749
34	582.8	10.2	949	13	BUI55689
35	581	10.2	910	13	BQ677666
36	580.4	10.2	941	13	BUI63307
37	575	10.1	602	10	BE043393
38	548.2	9.6	638	12	BM042282
39	541.8	9.5	546	14	CB118225
40	535.2	9.4	638	10	BE264293
41	530	9.3	563	10	AW295197
42	528.6	9.3	585	10	AW968546
43	528	9.2	528	14	CB158976
44	516.4	9.0	666	10	AW968720
45	498.2	8.7	509	10	AW504244

ALIGNMENTS

RESULT 1	BC012577	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.	2101 bp	mRNA	linear	HTC 04-MAR-2003
LOCUS	BC012577	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.	2101 bp	mRNA	linear	HTC 04-MAR-2003
DEFINITION	BC012577	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.	2101 bp	mRNA	linear	HTC 04-MAR-2003
ACCESSION	BC012577	BC012577	Homo sapiens, clone IMAGE:3996658, mRNA.	2101 bp	mRNA	linear	HTC 04-MAR-2003
VERSION	BC012577.1	BC012577.1	GI:15214876	2101 bp	mRNA	linear	HTC 04-MAR-2003
KEYWORDS	HTC	HTC	Homo sapiens (human)	2101 bp	mRNA	linear	HTC 04-MAR-2003
SOURCE	Homo sapiens	Homo sapiens	Homo sapiens	2101 bp	mRNA	linear	HTC 04-MAR-2003
ORGANISM	Homo sapiens	Homo sapiens	Homo sapiens	2101 bp	mRNA	linear	HTC 04-MAR-2003
REFERENCE	1	(bases 1 to 2101)	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	2101 bp	mRNA	linear	HTC 04-MAR-2003
AUTHORS	Strausberg, R.	Strausberg, R.	Strausberg, R.	2101 bp	mRNA	linear	HTC 04-MAR-2003
TITLE	Direct Submission	Direct Submission	Direct Submission	2101 bp	mRNA	linear	HTC 04-MAR-2003
JOURNAL	Submitted (15-AUG-2001)	Submitted (15-AUG-2001)	National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA	2101 bp	mRNA	linear	HTC 04-MAR-2003
REMARK	NIH-MGC Project URL: http://mgc.nci.nih.gov	NIH-MGC Project URL: http://mgc.nci.nih.gov	NIH-MGC Project URL: http://mgc.nci.nih.gov	2101 bp	mRNA	linear	HTC 04-MAR-2003
COMMENT	Contact: MGC help desk	Contact: MGC help desk	Contact: MGC help desk	2101 bp	mRNA	linear	HTC 04-MAR-2003
	Email: gcaps-rc@mail.nih.gov	Email: gcaps-rc@mail.nih.gov	Email: gcaps-rc@mail.nih.gov	2101 bp	mRNA	linear	HTC 04-MAR-2003
	Tissue Procurement: ATCC	Tissue Procurement: ATCC	Tissue Procurement: ATCC	2101 bp	mRNA	linear	HTC 04-MAR-2003
	cDNA Library Preparation: CLONTECH Laboratories, Inc.	cDNA Library Preparation: CLONTECH Laboratories, Inc.	cDNA Library Preparation: CLONTECH Laboratories, Inc.	2101 bp	mRNA	linear	HTC 04-MAR-2003
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	2101 bp	mRNA	linear	HTC 04-MAR-2003
	DNA Sequencing by: Institute for Systems Biology	DNA Sequencing by: Institute for Systems Biology	DNA Sequencing by: Institute for Systems Biology	2101 bp	mRNA	linear	HTC 04-MAR-2003
	http://www.systemsbio.org	http://www.systemsbio.org	http://www.systemsbio.org	2101 bp	mRNA	linear	HTC 04-MAR-2003
	contact: amadan@systemsbiology.org	contact: amadan@systemsbiology.org	contact: amadan@systemsbiology.org	2101 bp	mRNA	linear	HTC 04-MAR-2003

1805 DB CTAATTCAGAAATGAGAAAAATCTAAACCAATAGAAATCACTCGAAAAAGAAATCTGCTTTCA 1864
1861 QY AAAACGAAAGCTCAACCTATAAGCAGCAGTATTAAGCAATATGAATTCGAAATTAATATCC 1920
1865 DB AAAACGAAAGCTCAACCTATAAGCAGCAGTATTAAGCAATATGAATTCGAAATTAATATCC 1924
1921 QY ACAATTCAAAAGCACTAAAAGAAATAGCTCAGAGGAAAGTCTTCTACAGGCAATATTC 1980
1925 DB ACAATTCAAAAGCACTAAAAGAAATAGCTCAGAGGAAAGTCTTCTACAGGCAATATTC 1984
1981 QY ATGCGCTTGAACCTAGTACGATGAGAAATCTAAGCCCACTAATGTAATGCAATTCGAAA 2040
1985 DB ATGCGCTTGAACCTAGTACGATGAGAAATCTAAGCCCACTAATGTAATGCAATTCGAAA 2044
2041 QY TTGATAGTTGTTCTAGCAGTGAAGAGATAAAAGAAAAAGAAAGTACACCAAA 2091
2045 DB TTGATAGTTGTTCTAGCAGTGAAGAGATAAAAGAAAAAGAAAGTACACCAAA 2095

RESULT 2
BC030969
LOCUS
DEFINITION Homo sapiens, similar to breast cancer 1, early onset, clone
IMAGE:4804551, mRNA.
ACCESSION BC030969
VERSION BC030969.1 GI:21411299
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 2090)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (03-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapsb-remail.nih.gov
Tissue Procurement: DCTD/DTF
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LILNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www.shgc.stanford.edu>
Contact: {Dickson, Mark} mcdpaxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LILNL at: <http://image.llnl.gov>
Series: IRAL Plate: 41 Row: P Column: 11
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6552298
This clone has the following problem: frame shifted.

FEATURES
source
1..2090
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4804551"
/tissue_type="Prostate, adenocarcinoma."
/clone_lib="NIH MGC_60"
/lab_host="DH10B"
/note="Vector: pDNR-LIB"

ORIGIN

Query Match 36.0%; Score 2055.6; DB 11; Length 2090;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 2075; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 1 AGCTCGCTGAGACTTCTCGGACCCGACAGGCTGTGGGTTTCTCAGATAAATCGGACC 60
DB 2 AGCTCGCTGAGACTTCTCGGACCCGACAGGCTGTGGGTTTCTCAGATAAATCGGACC 60
QY 61 CCTCGGCTCAGAGGCTTCACTCTGCTCTGGTAAATTCATTCGACAGAAAGAAA 120
DB 61 CCTCGGCTCAGAGGCTTCACTCTGCTCTGGTAAATTCATTCGACAGAAAGAAA 120
QY 121 TGGATTATCTGCTCTTCTGGGTTGAGAGAGTACAAAATGTCAATTAATGCTATGACAGAAA 180
DB 121 TGGATTATCTGCTCTTCTGGGTTGAGAGAGTACAAAATGTCAATTAATGCTATGACAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTGCTCTGAGTGTGATCAAGGAACTGTCTCCAAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCCATCTGCTCTGAGTGTGATCAAGGAACTGTCTCCAAAAGTGTGACC 240
QY 241 ACATATTTTGC AAAATTTTGCATGCTGAACTTCTCAACCAAGAAAGGGGCTTCAAGT 300
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QY 301 GTCCTTTATGTAAGAATGATATAACCAAGAGGAGCTCAAGAAAGTACGAGATTATGTC 360
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QY 361 AACTGTGTGAGAGCTATGAAATATCATTTGTGCTTTTCAAGTGTGACACAGGTTGGAGT 420
DB 361 AACTGTGTGAGAGCTATGAAATATCATTTGTGCTTTTCAAGTGTGACACAGGTTGGAGT 420
QY 421 ATGCAAAACAGCTATATAATTTTGC AAAAAGGAAATAAATCTCTCTGAAACATCTAAAGATG 480
DB 421 ATGCAAAACAGCTATATAATTTTGC AAAAAGGAAATAAATCTCTCTGAAACATCTAAAGATG 480
QY 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540
DB 481 AAGTTTCTATCATCCAAAGTATGGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG 540
QY 541 AACCCGAAAATCCCTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAAACCTTGAA 600
DB 541 AACCCGAAAATCCCTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAAACCTTGAA 600
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QY 661 AATTGGGATCTGATTTCTTGAAGATACCTGTTAATAAGSCAACTTATTGACAGTCTGGAG 720
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QY 721 ATCAAGAAATTTTACAAATCACTCCCTCAAGGAAACCGAGGATGAAATCAGTTTGGATTCTG 780
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DB 841 CCAGTAATAATGATTTTGAACACCACTCAGAGAGCGTGCGAGCTGAGAGGCATCCAGAAAGT 900
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QY 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCCGACAGAAAAAAGGTAG 1140
Db 1081 GGGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCCGACAGAAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAAGTAAAGTAAAGCAGAACTCCCATGCT 1200
Db 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGAAAGTAAAGTAAAGCAGAACTCCCATGCT 1200
QY 1201 CAGAGAACTCAGAGTACTGAGAGTTCCTTGGATTAACACTAAATAGCAGCAATTCAGA 1260
Db 1201 CAGAGAACTCAGAGTACTGAGAGTTCCTTGGATTAACACTAAATAGCAGCAATTCAGA 1260
QY 1261 AAGTAAATGAGTGGTTTCCAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
Db 1261 AAGTAAATGAGTGGTTTCCAGAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 1320
QY 1321 GGGAGTCTGAATCAATGCGAAAGTACTGATGATGATGATGATGATGATGATGATGATGATG 1380
Db 1321 GGGAGTCTGAATCAATGCGAAAGTACTGATGATGATGATGATGATGATGATGATGATGATG 1380
QY 1381 AATATTCTGCTTCTCAGAGAAATAGACTTACTGCGCAGTGTACTCTCATGAGGCTTTAA 1440
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QY 1441 TATGTAAGTGAAGAGTTCATCCAAATCAGTACAGAGTAAATATGGAAGCAAAATAT 1500
Db 1441 TATGTAAGTGAAGAGTTCATCCAAATCAGTACAGAGTAAATATGGAAGCAAAATAT 1500
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Db 1501 TTGGGAAACCTATCCGAGAGGCGCAAGCTCCCAACTTACCCCACTGATGATGATGATGATG 1560
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QY 1621 AATTAAGGCTAAAGAGACCTACATCAGGCTTCATCTCAGTAAATATTAATCAAGAAAG 1680
Db 1621 AATTAAGGCTAAAGAGACCTACATCAGGCTTCATCTCAGTAAATATTAATCAAGAAAG 1680
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QY 1741 AGAATGCTCAGTATGATATATTAATGATGCTGATGATGATGATGATGATGATGATGATGAT 1800
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QY 1801 CTATTGAGATGAGAAATCTTAACCCCAATAGATCACTCGAAGAAAGATCTGCTTTCA 1860
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QY 1861 AAACGAAAGCTGAACTTAAAGCAGTATTAAGCAATATGAACTCGAATTAATATATCC 1920
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QY 1981 ATGCGCTTGAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2040
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QY 2041 TTGATAGTGTCTTACGAGTGAAGATTAAGAAAAAAGTAAACCA 2090
Db 2041 TTGATAGTGTCTTACGAGTGAAGATTAAGAAAAAAGTAAACCA 2090
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RESULT 3
BC038947
LOCUS BC038947 1578 bp mRNA linear HTC 04-MAR-2003
DEFINITION Homo sapiens, similar to breast cancer 1, early onset, clone

IMAGE:5531286, mRNA.
BC038947
VERSION BC038947.1 GI:25058570
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1578)
Strausberg, R.
Direct Submission
Submitted (01-NOV-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc_mgc@nslri.nih.gov
Akter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgren, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: TRAK Plate: 82 Row: 9 Column: 3
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 6552304
This clone has the following problem: retained intron.

Location/Qualifiers
1..1578
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/db_xref="taxon:9606"
/clone="IMAGE:5531286"
/tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
/lab_host="DH10B"
/note="vector: pCW-SPORT6"

ORIGIN

Query Match 24.8%; Score 1416.4; DB 11; Length 1578;
Best Local Similarity 92.5%; Pred. No. 1.8e-311;
Matches 1563; Conservative 0; Mismatches 1; Indels 126; Gaps 2;

QY 391 GTGCTTTTCAGCTTGACACAGGTTTGAGTATGCAACAGCTATAATTTGCAAAAAGG 450
Db 12 GTGCTTTTCAGCTTGACACAGGTTTGAGTATGCAACAGCTATAATTTGCAAAAAGG 71

QY 451 AAAATAACTCTCCGACATCAAAAGATGAAGTTTCTATCTATCTCAAGTATGGCTACA 510
Db 72 AAAATAACTCTCCGACATCAAAAGATGAAGTTTCTATCTATCTCAAGTATGGCTACA 131

QY 511 GAAACCGTGCCAAAGACTTCTACAGAGTGAACCCGAAATCTCTTCCTTCAGGAAACCA 570
Db 132 GAAACCGTGCCAAAGACTTCTACAGAGTGAACCCGAAATCTCTTCCTTCAGGAAACCA 188

QY 571 GTCTCAGTGTCCAACTCTCTAACTTGGAACTGTGAGAACTCTGAGGACAAAGCAGGA 630
Db 189 GTCTCAGTGTCCAACTCTCTAACTTGGAACTGTGAGAACTCTGAGGACAAAGCAGGA 248

5 The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)

6 (bases 1 to 1919)
Adachi,J., Aizawa,K., Akimura,T., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Furuno,M., Hangaki,T., Hara,A., Hashizume,W., Hayashida,K., Hayatsu,M., Hiramoto,K., Hiraoka,T., Hirozane,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Kagawa,I., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Kondo,S., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Murata,M., Nakamura,M., Nishi,K., Nomura,K., Numasaki,R., Ono,M., Ohsato,N., Okazaki,Y., Saiko,R., Saitoh,H., Sakai,C., Sakai,K., Sakazume,N., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sugabe,Y., Tagami,M., Tagawa,A., Takahashi,F., Takaku-Akahira,S., Takeda,Y., Tanaka,T., Tomaru,A., Toya,T., Yasunishi,A., Muramatsu,M. and Hayashizaki,Y.

Direct Submission
Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.go.jp, URL: <http://genome.gsc.riken.go.jp/>, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL: <http://genome.gsc.riken.go.jp/>
URL: <http://fantom.gsc.riken.go.jp/>.
Location/Qualifiers
1. 1919
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM,DB:D930010H15"
/db_xref="MGI:2423542"
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/clone="D930010H15"
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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note="breast cancer 1 (MGD|MGI:104537, GB|U36475, evidence: BLASTN, 99%, match=1499)
putative"

misc_feature
Query Match 17.0%; Score 968.8; DB 11; Length 1919;
Best Local Similarity 73.5%; Pred. No. 1.7e-209;
Matches 1384; Conservative 0; Mismatches 387; Indels 113; Gaps 7;

ORIGIN
QY 57 GGCCCTCGCGTCAGAGGCGCTTCACCCCTCTGCTCGGTTAAAGTTTCATTGGAAACAGAAA 116
DB 146 GTCTCGCGCGCTTGGAAAGTAGCGGATCTTTTCTCGGAGAAAAGTCTCACTGGAACCTGAA 205
QY 117 GAATGGAATTATCTGCTCTTCGCGGTGAAGAGATCAAAATGCTTAATGCTATGCGAG 176
DB 206 GAAATGGAATTATCTGCGCGTCCAAATTCAGAAAGTACAAATGTGCTTCATGCTATGCGAG 265
QY 177 AAAATCTTAGAGTGCCCATCTGTCGTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGT 236
DB 266 AAAATCTTAGAGTGTCCGAGCTGTTTGGACTGATCAAGAACTGTTTTCACAAAGTGT 325
QY 237 GACCACATATTTGCCAAATTTTGATGCTGAAACTTCTTCACACGAGAAAGGCGCTTCA 296
DB 326 GACCACATATTTGCCAAATTTTGATGCTGAAACTTCTTACACGAGAAAGGCGCTTCA 385

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Db 1368 GATGGGGTTTGTAGTCTTCAAGGAACACAGACTAGTAACCCCGACCCCATCTACT 1427
Qy 1437 TTAATATGTAAGTGAAGAGTTCACTCCAAATCAGTAGAGAGTAATATTGAACAAA 1496
Db 1428 TTAATGTGTAAAGTGAAGAGACTTCTCCAAACACAGTAGAGAGTAATATCAGTGATAA 1487
Qy 1497 ATATTGGGAACCTATCGGAGAGGCAAGCCTCCCACTTAAGCCATGTAACCTAA 1556
Db 1488 ATATTGGGAATCTTATCAGGAAGGAGAGCGCCCTCACTGAACTGTGACTGA- 1546
Qy 1557 AATCTAATATAGGAGCAATTTGTTACTGAGCCACAGATAATAACAGAGCGTCCCTCA 1616
Db 1547 -----AATTATAGGCACATTATTATCAGAAACACAGATAACACAGAGCAGCCCTCA 1601
Qy 1617 AATAAATTAAAGCTTAAGGAGAGACTCATCAGAGCCTTCACTCTGAGGATTTATCAAG 1676
Db 1602 AATAAATTAAACGTAAGAGAG-----TATCTCCCTTCAACCTTGAGACTTTCATCA 1655
Qy 1677 AAAGCAGATTTGGCA---GTTCAAAAGACTCTCTGAATGATAAATCAGGGAACCTAACCA 1733
Db 1656 AAAGCAGATTCAGCAGGTGTTCAAAGGACTCTGACAACTAATAATCAGGGAACCTGACCTA 1715
Qy 1734 AGGAGCAGAAATGTTCAAGTGAATATTAATATGTTGTTCAATGAGAGTAATAACAAA 1793
Db 1716 ATGGAGCCAAATGAGCAGCAGTGAATACCTACCTGTAATCTGTCAGGAGAACTAATGA 1775
Qy 1794 GGTGATTTCTATTCAGATGAGAAATCTTACCAATAGATCACTCGAAAGAACTCT 1853
Db 1776 GGTAGTAATCTCCAGAGAGAAAGCGCTCATCCAACTGATCACTTGAAGAGAACTCT 1835
Qy 1854 GCTTTCAAAACGAAAGCTGAACCTATAGCAGCAGTATTAAGCAATATGGAACCTGAAATTA 1913
Db 1836 GCTTCCACAGCAGGAGCCAAATCTATAAGCAACAGTGAAGTGAATTTGGAGTGAATTA 1895
Qy 1914 AATATCCCAATTTCAAAAGCAGCT 1937
Db 1896 AACGTCACAGTTCAAAAGCAGCT 1919
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RESULT 5
LOCUS BQ068830
DEFINITION AGENCOURT_6740238 NIH_MGC_47 Homo sapiens cDNA clone IMAGE:5802685
5', mRNA sequence.
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ACCESSION BQ068830
VERSION BQ068830.1 GI:19897888
KEYWORDS EST.
SOURCE Homo sapiens (human)
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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REFERENCE 1 (bases 1 to 962)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
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Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
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http://image.llnl.gov
Plate: LLCW2037 row: h column: 14
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Location/Qualifiers
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/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_47"
/notes="Organ: Brain; Vector: pOTB7; Site: 1: XhoI; Site: 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCACGAG(G). Size-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."
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ORIGIN

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Query Match 15.1%; Score 863; DB 13; Length 962;
Best Local Similarity 96.3%; Pred. No. 1.8e-185;
Matches 891; Conservative 0; Mismatches 32; Indels 2; Gaps 1;

Qy 4451 TCCAGAACAAAGCAGCATCAGAAAAAGCAGTAATTAATCTTCAGAAAAAGTAGTGAATACCC 4510
Db 15 TTCCGCCACGAGGCACATCAGAAAAAGCAGTAATTAATCTTCAGAAAAAGTAGTGAATACCC 74
Qy 4511 TATAGCCAGAAATCCAGAGGCCCTTCTGCTGACAGTCTTGGAGTGTCTGCAGATAGTTC 4570
Db 75 TATAGCCAGAAATCCAGAGGCCCTTCTGCTGACAGTCTTGGAGTGTCTGCAGATAGTTC 134
Qy 4571 TACCAGTAAATAAATAAGAACCCAGAGTGGAAAGTCTATCCCTTCTTAATGCCCATCAT 4630
Db 135 TACCAGTAAATAAATAAGAACCCAGAGTGGAAAGTCTATCCCTTCTTAATGCCCATCAT 194
Qy 4631 AGATGATAGTGGTACATGACAGTCTGCTCTGGAGTCTTCAGATAGAACTACCCATC 4690
Db 195 AGATGATAGTGGTACATGACAGTCTGCTCTGGAGTCTTCAGATAGAACTACCCATC 254
Qy 4691 TCAAGAGAGTCTCAATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAGAGTCTGGGCC 4750
Db 255 TCAAGAGAGTCTCAATTAAGGTTGTTGATGTGGAGGAGCAACAGCTGGAAGAGTCTGGGCC 314
Qy 4751 ACAGATTTGACGGAACATCTTACTTGCAGACAGTCTAGAGGAGGAGCCCTTACCT 4810
Db 315 ACAGATTTGACGGAACATCTTACTTGCAGACAGTCTAGAGGAGGAGCCCTTACCT 374
Qy 4811 GGAATCTGGAAATCAGCTCTTCTCTGATGACCTCTGATCTGATCTCTCTGAAGACAGC 4870
Db 375 GGAATCTGGAAATCAGCTCTTCTCTGATGACCTCTGATCTGATCTCTCTGAAGACAGC 434
Qy 4871 CCCAGAGTCACTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGAAAGTTCCCA 4930
Db 435 CCCAGAGTCACTGCTGTTGGCAACATACCATCTTCAACCTCTGCAATGAAAGTTCCCA 494
Qy 4931 ATTGAAGTTGCAAGATCTGCCAGGCTCCAGCTGCTGCTCATCTACTACTGCTGCTGG 4990
Db 495 ATTGAAGTTGCAAGATCTGCCAGGCTCCAGCTGCTGCTCATCTACTACTGCTGCTGG 554
Qy 4991 GTATAATGCAATGGAAGAAAGTGTGACGAGGAGAGCCAGAAATTTGACGCTTCAACAGA 5050
Db 555 TTATAATGCAATGGAAGAAAGTGTGACGAGGAGAGCCAGAAATTTGACGCTTCAACAGA 614
Qy 5051 AAGGTTCAACAAAGATGTCATGTTGGTGTCTGGCTGACCCAGAGAAATTTATGCT 5110
Db 615 AAGGTTCAACAAAGATGTCATGTTGGTGTCTGGCTGACCCAGAGAAATTTATGCT 674
Qy 5111 CGTGTAAGAATTTGCCAGAAAAACACCATCATCTTTAACTAACTAATTAATCTGAAGAGAC 5170
Db 675 CGTGTAAGAATTTGCCAGAAAAACACCATCATCTTTAACTAATTAATCTGAAGAGAC 734
Qy 5171 TACTCATGTTGTTATGAAAAACAGATGCTGAGTGTGTGTGTAACCGACACTGAATATT 5230
Db 735 TACTCATGTTGTTATGAAAAACAGATGCTGAGTGTGTGTGTAACCGACACTGAATATT 794
Qy 5231 TCTAGGAATTTGGGAGGAAAAATGGGTAGTGTAGTCTATTTCTGGGTGACCCAGCTCTATTA 5290
Db 795 TCTAGGAATTTGGGAGGAAAAATGGGTAGTGTAGTCTATTTCTGGGTGACCCAGCTCTATTA 854
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Db 241 GTRAAATATACCTCTCAGTCTACTAGGATAGACACCGTGTCTCCGAGTGTCTGTCT 300
Qy 3879 AAGAACACAGAGGAGAGATTTATTCATTTGAAGATAGCTTTAAATGACTGACGTAACCCAG 3938
Db 301 AAGAACACAGAGGAGAGATTTATTCATTTGAAGATAGCTTTAAATGACTGACGTAACCCAG 360
Qy 3939 GTATATTTGGCAAGGAGCTCTCAGAACATCACCTTAGTGAGGAAACAAATGTTCTGCT 3998
Db 361 GTAATTTGGCAAGGAGCTCTCAGAACATCACCTTAGTGAGGAAACAAATGTTCTGCT 420
Qy 3999 AGCTTGTGTTTCTTCAAGTGCAGTGAATTTGAAGACTTGTACTGCAAAATACAAACACCCAG 4058
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Qy 4059 GATCCTTTCTGATTTGTTCTTCCAAACAAATGAGGAGCTAGTCTGAAGCCAGGGAGTT 4118
Db 481 GATCCTTTCTGATTTGTTCTTCCAAACAAATGAGGAGCTAGTCTGAAGCCAGGGAGTT 540
Qy 4119 GGTCTGAGTGCACAGGAATTTGTTTTCAGATGATGAAGAAAGAGGAAACGGGCTTGGAGAA 4178
Db 541 GGTCTGAGTGCACAGGAATTTGTTTTCAGATGATGAAGAAAGAGGAAACGGGCTTGGAGAA 600
Qy 4179 AATATCAAGAGAGCAAGGAGTGAATTCATTAAGCTTTAGTGAAGCGCATCTGGGTGTGAG 4238
Db 601 AATATCAAGAGAGCAAGGAGTGAATTCATTAAGCTTTAGTGAAGCGCATCTGGGTGTGAG 660
Qy 4239 AGTGAACACAGGCTCTCTGAAGACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAA-C 4297
Db 661 AGTGAACACAGGCTCTCTGAAGACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAA-C 720
Qy 4298 CACTCAGCAGAGGAGTACATGCAATCAATCACTGATAAGCTCCAGCAGGAAATGGCTGA 4357
Db 721 CACTCAGCAGAGGAGTACATGCAATCAATCACTGATAAGCTCCAGCAGGAAATGGCTGA 780

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RESULT 9

CK000353
LOCUS
DEFINITION AGENCOURT_16368380 NIH_MGC_220 Homo sapiens cDNA clone
IMAGE:30706752 5', mRNA sequence.

ACCESSION

CK000353

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 789)

AUTHORS

NIH-MGC <http://mgi.nci.nih.gov/>

TITLE

National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL

Unpublished (1999)

COMMENT

Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgaabs-remail.nih.gov
Tissue Procurement: James Martin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
DNA Sequencing by: The I.M.A.G.E. Consortium (ILLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/ILLNL at:
<http://image.llnl.gov>
Plate: NDAM1070 row: e column: 01
High quality sequence stop: 713.
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/db_xref="taxon:9606"
/clone="IMAGE:30706752"
/lab_host="DH10B fona"

FEATURES

source

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/clone lib="NIH_MGC_220"
/note="Organ: mixed; Vector: pYX-Asc; Site 1: EcoRI;
Site 2: NotI; Library is oligo-dT primed and directionally
cloned. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to RNA size fraction, ligated with
EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. Average insert size
0.5-1kb. Adaptors 5' (AATTCGGACGAGG)3' and 5' (
CTCTGCGCG)3'. 3' linker sequence - GCGCCGCTGAGGCC T18.
Sequencing primers 3' end: T3 promoter primer 5' (
AATTAACCTCACTAAGGGA)3'. 5' End: T7 promoter primer 5' (
TAATACGACTCACTATAGG)3'. Library was constructed in the
laboratory of M. Bento Soares. Average insert size 3-4kb
Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match 13.1%; Score 750.6; DB 14; Length 789;
Best Local Similarity 99.3%; Pred. No. 6.9e-160;
Matches 764; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

Qy 3185 AGTGAGCACAAATTAGCGTAATTAACATTAGAGAAATGTTTAAAGGAGCCAGCTCAAG 3244
Db 5 AGGAGCACAAATTAGCGTAATTAACATTAGAGAAATGTTTAAAGGAGCCAGCTCAAG 64
Qy 3245 CAATATTAAATGAAGTAGTTCCTAGTACTAATGAAGTGGCTCCAGTATTAAATGAATAGG 3304
Db 65 CAATATTAAATGAAGTAGTTCCTAGTACTAATGAAGTGGCTCCAGTATTAAATGAATAGG 124
Qy 3305 TTCCAGTGAGAAACATTTCAAGCAGACATAGTGTGAAGACAGAGGGCCAAATTTGAATGC 3364
Db 125 TTCCAGTGAGAAACATTTCAAGCAGACATAGTGTGAAGACAGAGGGCCAAATTTGAATGC 184
Qy 3365 TATGCTTAGATTAGGGGTTTTCGAACTGAGGTTCTATAACAAAGTCTTCTCTGGAAGTAA 3424
Db 185 TATGCTTAGATTAGGGGTTTTCGAACTGAGGTTCTATAACAAAGTCTTCTCTGGAAGTAA 244
Qy 3425 TTGTAGCATCTCTGAATAAATAAAGACAGAAATAGAAAGTAGTTCAGAGCTGTAAATAC 3484
Db 245 TTGTAGCATCTCTGAATAAATAAAGACAGAAATAGAAAGTAGTTCAGAGCTGTAAATAC 304
Qy 3485 AGATTTCTCTCCATATCTGATTTTTCAGATACTTAGAACACAGCTATGGAAGTAGTCTATGC 3544
Db 305 AGATTTCTCTCCATATCTGATTTTTCAGATACTTAGAACACAGCTATGGAAGTAGTCTATGC 364
Qy 3545 ATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTAGATGATGTTGTAATAAAGGAAGA 3604
Db 365 ATCTCAGGTTTGTCTGAGACACCTGATGACCTGTGTAGATGATGTTGTAATAAAGGAAGA 424
Qy 3605 TACTAGTTTGTCTGAAATGACATTTAGGAAAGTCTGCTGTTTGTAGCAAAAGCGTCCA 3664
Db 425 TACTAGTTTGTCTGAAATGACATTTAGGAAAGTCTGCTGTTTGTAGCAAAAGCGTCCA 484
Qy 3665 GAGAGGAGAGCTTAGCAGGAGTCTCTAGCCCTTTTCCACCCATACACATTTGGCTCAGGGTTA 3724
Db 485 GAGAGGAGAGCTTAGCAGGAGTCTCTAGCCCTTTTCCACCCATACACATTTGGCTCAGGGTTA 544
Qy 3725 CCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATGAAGA 3784
Db 545 CCGAAGAGGGGCCAAGAAATTAGAGTCTCTCAGAGAGAACTTATCTAGTGAGGATGAAGA 604
Qy 3785 GCTTCCCTGCTTCCAAACATTTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGTCTAC 3844
Db 605 GCTTCCCTGCTTCCAAACATTTGTTTATTTGGTAAAGTAAACAATATACCTTCTCAGTCTAC 664
Qy 3845 TAGGCATAGCACCGTCTCTACCGAGTCTCTGTCTAGAAACACAGAGAGGATTTTATTC 3904
Db 565 TAGGCATAGCACCGTCTCTACCGAGTCTCTGTCTAGAAACACAGAGAGGATTTTATTC 724
Qy 3905 ATTGAGAGATAGCTTTAAATGACTGCACTAACCCAGGTAAATTTGGCAAG 3953
Db 725 ATTGAGAGATAGCTTTAAATGACTGCACTAACCCAGGTAAATTTGGCAAG 772

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RESULT 10
LOCUS      BUI71200
DEFINITION AGENCOURT_7956206 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6161612
5', mRNA sequence.
ACCESSION  BUI71200
VERSION     BUI71200.1 GI:22685184
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE   1 (bases 1 to 933)
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTF
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Agencourt Bioscience Corporation
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM1514 row: c column: 21
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            Location/Qualifiers
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                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 2 kb. Library constructed by Life
                Technologies."
ORIGIN
Query Match      13.1%; Score 746.4; DB 13; Length 933;
Best Local Similarity 98.3%; Pred. No. 6.5e-159;
Matches 765; Conservative 0; Mismatches 11; Indels 2; Gaps 1;
QY 4709 GGTGTTGATGTGGAGGAGCAGCTGGAGAGTCTGGGCCACACGATTTGACGGAAC 4768
DB 12 GGTGTTGATGTGGAGGAGCAGCTGGAGAGTCTGGGCCACACGATTTGACGGAAC 71
QY 4769 ATCTTACTTGCAGGCAAGATCTAGAGGAAACCCCTTACCTGGAATCTGGAATCAGCCT 4828
DB 72 ATCTTACTTGCAGGCAAGATCTAGAGGAAACCCCTTACCTGGAATCTGGAATCAGCCT 131
QY 4829 CTTCCTGATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 4888
DB 132 CTTCCTGATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
QY 4889 TGGCAACATACATCTTCAACTCTGCAATGGAAGTCCCAATTTGAAAGTTGCAAGATC 4948
DB 192 TGGCAACATACATCTTCAACTCTGCAATGGAAGTCCCAATTTGAAAGTTGCAAGATC 251
QY 4949 TGCCAGGAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 5008
DB 252 TGCCAGGAGTCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 311
QY 5009 AAGTGTGAGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5068
DB 312 AAGTGTGAGCGGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 371
QY 5069 GTCCATGTGTGTCTGGCCCTGACCCAGAGAAATTTATGCTGTGTACAAAGTTTGCCAG 5128
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DB 372 GTCCATGTGTGTCTGGCCCTGACCCAGAGAAATTTATGCTGTGTACAAAGTTTGCCAG 431
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DB 432 AAAACACACACATCACTTTTAACTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 491
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DB 492 AACAGATGCTGAGTTGTGTGTGAACGGACACATGAAATATTTTCTAGGAATTCGGGAGG 551
QY 5249 AAAATGGTGTAGTGTATTTCTGGGTGACCCAGTCTTATTAAAGAAAGAAAATGCTGAA 5308
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QY 5429 GCCCTTCCACACATGCCACAG--ATCAACTGGAATGGATGGTACAGCTGTGTGGTG 5484
DB 732 GCCCTTCCACACATGCCACAGNNATCACTGGGAATGGATGGGTACAGCTGTGGTG 789
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LOCUS      BG681276
DEFINITION 602627125F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4751887 5',
mRNA sequence.
ACCESSION  BG681276
VERSION     BG681276.1 GI:13912673
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
            NIH-MGC http://mgi.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-remail.nih.gov
            Tissue Procurement: James Cleaver, M.D.
            cDNA Library Preparation: Life Technologies, Inc.
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LHAM10609 row: a column: 08
            High quality sequence stop: 741.
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                Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert size 1.5kb. Library constructed by Life
                Technologies. Note: this is a NCI_CGAP Library."
ORIGIN
Query Match      12.9%; Score 738.8; DB 12; Length 743;
Best Local Similarity 99.7%; Pred. No. 3.3e-157;
Matches 740; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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4724 GGAGCAACAGCTGGAGAGCTGGGSCACACGATTGGACGAAACATCTTACTGCCAAG 4783
1 GGAGCAACAGCTGGAGAGCTGGGSCACACGATTGGACGAAACATCTTACTGCCAAG 60
4784 GCAAGATCTAGAGGGAACCCCTTACTGGAAATCTGGAATTCAGCCCTCTTCTGTGATGACCC 4843
61 GCAAGATCTAGAGGGAACCCCTTACTGGAAATCTGGAATTCAGCCCTCTTCTGTGATGACCC 120
4844 TGAATCTGATCTCTTCTGAGACAGAGCCCCAGAGTCAGCTGTGTCGCAACATACCATC 4903
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5384 CCAGGACAGAAAGATCTTCAGGGGCTAGAAATCTGTTGCTATGGGCCCCCTTCACCAAT 5443
661 CCAGGACAGAAAGATCTTCAGGGGCTAGAAATCTGTTGCTATGGGCCCCCTTCACCAAT 720
5444 GCCACAGATCAACTGGAATGG 5465
721 GCCACAGATCAACTGGAATGG 742

RESULT 12

BQ422380
LOCUS AGENCOURT_7802085 NIH_MGC_92 Homo sapiens cdna clone IMAGE:6042052
DEFINITION 5' mRNA sequence. EST 23-MAY-2002

ACCESSION BQ422380
VERSION BQ422380.1 GI:21117695
KEYWORDS EST.

SOURCE Homo sapiens
ORGANISM Homo sapiens (human)

REFERENCE 1 (bases 1 to 899)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC

cdna Library Preparation: Life Technologies, Inc.
cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLAM13280 row: n column: 05
High quality sequence stop: 597.

FEATURES

source

1..899
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/lab_host="DH10B (phage-resistant)"
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/note="Organ: testis; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 2.5 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

ORIGIN

Query Match 12.9% Score 734.6; DB 13; Length 899;
Best Local Similarity 97.1%; Pred. No. 3.1e-156;
Matches 824; Conservative 0; Mismatches 11; Indels 14; Gaps 7;
QY 30 CAGGCTGTGGGTTTCTCAGATAACCTGGGCGCTCGCTCAGGAGGCTTCACCTCTGC 89
DB 16 CAGGCTGTGGGTTTCTCAGATAACCTGGGCGCTCGCTCAGGAGGCTTCACCTCTGC 75
QY 90 TCTGGGTAAAGTTTCATTTGGACAGAAAGAAATGATTTATCTGCTTCGCGTTGAAGAA 149
DB 76 TCTG-----GTTTCATTTGGACAGAAAGAAATGATTTATCTGCTTCGCGTTGAAGAA 129
QY 150 GTACAAATGTCTAATATGCTATGACAGAAATCTTAGAGTGTCCATCTGTCTGAGTTG 209
DB 130 GTACAAATGTCTAATATGCTATGACAGAAATCTTAGAGTGTCCATCTGTCTGAGTTG 189
QY 210 ATCAAGGACCTGTCTCCACAAAGTGTGACACATATTTGCAATTTTCGATCTGAAA 269
DB 190 ATCAAGGACCTGTCTCCACAAAGTGTGACACATATTTGCAATTTTCGATCTGAAA 249
QY 270 CTCTCAACAGAGAAAGGCGCTTCACAGTGTCTTTATGTAAGAAATGATATACCAA 329
DB 250 CTCTCAACAGAGAAAGGCGCTTCACAGTGTCTTTATGTAAGAAATGATATACCAA 309
QY 330 AGGAGCTTACAGAAAGTACGAGATTTAGTCACTTGTGGAAGAGCTATTGAAATCAT 389
DB 310 AGGAGCTTACAGAAAGTACGAGATTTAGTCACTTGTGGAAGAGCTATTGAAATCAT 369
QY 390 TGTGCTTTTCAGCTTGTGACACAGGTTTGGAGTGTGCAACAGCTATATTTTGCAGAAAG 449
DB 370 TGTGCTTTTCAGCTTGTGACACAGGTTTGGAGTGTGCAACAGCTATATTTTGCAGAAAG 429
QY 450 GAAATAACTCTCTGCAACATCTTAAAGATGAAAGTTTCTATCTATCCAAAGATGGCTAC 509
DB 430 GAAATAACTCTCTGCAACATCTTAAAGATGAAAGTTTCTATCATCCAAAGATGGCTAC 489
QY 510 AGAAGCCGTGCCAAAGAGCTTCTACAGAGTGAACCCGAAATCTCTCTCCGTCAGAGAAAC 569
DB 490 AGAAGCCGTGCCAAAGAGCTTCTACAGAGTGAACCCGAAATCTCTCTCTCTCTCTCTCT 546
QY 570 AGTCTGAGTGTCCAACTCTCTTAACCTTGGAACTGTGAGAACTCTGAGGACAAAGACGG 629
DB 547 AGTCTGAGTGTCCAACTCTCTTAACCTTGGAACTGTGAGAACTCTGAGGACAAAGACGG 606
QY 630 ATACAGCTCAAAAGAGCTCTGCTACATTTGAATGGATCTGATTTCTCTGAGATACC 689
DB 607 ATACAGCTCAAAAGAGCTCTGCTACATTTGAATGGATCTGATTTCTCTGAGATACC 666
QY 690 GTTAATAAGGCAACTTATTTCAGTGTGGGAGATCAAGAAATGTTTACAAATCACCCTCAA 749

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Db      667 GTTAATAGGCAACTTATTCAGTGTGGAGATCAAGANTGTACAAATCAACCCCTCAA 726
Qy      750 GGAACCA-GGGATCAATCAGTTGGATTCTGCAGAAAGAGCTGC-TTGGAATTTCTG 807
Db      727 GGAACCAAGGATCAATCAGTTGGATTCTGCAGAAAGAGCTGC-TTGGAATTTCTG 786
Qy      808 AGACGGATGAACA-ATACCTGACATC-ATCAACCCAGTAATAATGA-TTTCACACCA 864
Db      787 AGACGGATGTACAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCAATCA 846
Qy      865 CTGAGAGC 873
Db      847 CTGAGAAC 855

RESULT 13
BO215100 878 bp mRNA linear EST 02-MAY-2002
LOCUS AGENCOURT 7591049 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6065516
DEFINITION 5', mRNA sequence.
ACCESSION BO215100
VERSION BO215100.1 GI:20396500
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 878)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cga@bbs-remail.nih.gov
Tissue Procurement: ATCC/DCTb/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1AM13341 row: 0 column: 21
High quality sequence stop: 669.
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location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:6065516"
/tissue_type="melanotic melanoma"
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/note="Organ: skin; Vector: pCMV-SPORT6; Site: 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dr.
Average insert size 2 kb. Library constructed by Life
Technologies."

ORIGIN
Query Match 12.4%; Score 706.2; DB 13; Length 878;
Best Local Similarity 98.8%; Pred. No. 9.2e-150;
Matches 754; Conservative 0; Mismatches 3; Indels 6; Gaps 4;

Qy      30 CAGGCTGGGGTTTCTCAGATACTGGCCCTCGGCTCAGGAGGCTTCACCCCTGCG 89
Db      13 CAGGCTGGGGTTTCTCAGATACTGGCCCTCGGCTCAGGAGGCTTCACCCCTGCG 72
Qy      90 TCTGGGTAAGTTCATTGGACACAGAAAGAAATGATTATCTGCTTCGGTTGAAGAA 149
Db      73 TCTGGGTAAGTTCATTGGACACAGAAAGAAATGATTATCTGCTTCGGTTGAAGAA 132
Qy      150 GTACAAATGTCATATGCTATCGCAAAATCTTAGAGTCCCATCTGCTGAGTTG 209
Db      133 GTACAAATGTCATATGCTATCGCAAAATCTTAGAGTCCCATCTGCTGAGTTG 192

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Qy      210 ATCAGGACCTGTCTCCACAAAGTGTGACACATATTTTGCATAATTTTGCATGCTGAAA 269
Db      193 ATCAGGAACTGTCTCCACAAAGTGTGACACATATTTTGCATAATTTTGCATGCTGAAA 252
Qy      270 CTTCTCAACACAGAAAGAGGGCTTCACAGAGTCTCTTTATGTAAGAAATGATATAACCAA 329
Db      253 CTTCTCAACACAGAAAGAGGGCTTCACAGAGTCTCTTTATGTAAGAAATGATATAACCAA 312
Qy      330 AGAGGCTTACAGAAAGTACGAGATTAGTCAACTGTTGTAAGAGCTATTGAAATCATTT 389
Db      313 AGAGGCTTACAGAAAGTACGAGATTAGTCAACTGTTGTAAGAGCTATTGAAATCATTT 372
Qy      390 TGTGCTTTTTCAGCTTGACACAGCTTTGGAGTAGTGCACACAGCTATAATTTTGCATAAAG 449
Db      373 TGTGCTTTTTCAGCTTGACACAGCTTTGGAGTAGTGCACACAGCTATAATTTTGCATAAAG 432
Qy      450 GAAATATACCTCTCTGAAACATCTAAAGAGTGTATGAGTTTCTATCATCCAAAGTAGTGGCTAC 509
Db      433 GAAATATACCTCTCTGAAACATCTAAAGAGTGTATGAGTTTCTATCATCCAAAGTAGTGGCTAC 492
Qy      510 AGAAACCGTGCACAAAGAGCTTCTACAGAGTGAACCCGAAATCTCTTCCTTCGAGGAAACC 569
Db      493 AGAAACCGTGCACAAAGAGCTTCTACAGAGTGAACCCGAAATCTCTTCCTTCGAGGAAACC 549
Qy      570 AGTTCAGTGTCAACTCTTAACCTTGAACCTGTGAGAACTCTGAGGACAAAGCAGCGG 629
Db      550 AGTTCAGTGTCAACTCTTAACCTTGAACCTGTGAGAACTCTGAGGACAAAGCAGCGG 609
Qy      630 ATACACCTCAAAAGAGCTGTCTACATTGAATTTGGAGTCTGATTTCTTCTGAGATACC 689
Db      610 ATACACCTCAAAAGAGCTGTCTACATTGAATTTGGAGTCTGATTTCTTCTGAGATACC 669
Qy      690 GTTAATAAGCCAACTTATTGTCAGT-GTGGAGATCAAGAAATGTTTACAAATCACCCCTCA 748
Db      670 GTTAATAAGCCAACTTATTGTCAGTGTGGAGATCAAGAAATGTTTACAAATCACCCCTCA 729
Qy      749 AGGAACCA-GGATGAATCAG-TTGGATCTTCGAAAAAGS 789
Db      730 AGGACCAAGGGATGAATCAGTTTGGATTCTGCAAAAAAG 772

RESULT 14
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LOCUS UI-RP-BPop-arn-g-04-0-UI.r1 NIH_MGC_51 Homo sapiens cDNA clone
DEFINITION IMAGE:30566859 5', mRNA sequence.
ACCESSION CF121736
VERSION CF121736
KEYWORDS EST.
SOURCE CF121736.1 GI:33194237
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 739)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLES Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
PUBMED 8889548
COMMENT Contact: Soares, MB
Coordinated Laboratory for Computational Genomics
University of Iowa
375 Newton Road, 4156 MEERF, Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
Tissue Procurement: Louis Scaud
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at

```

http://genome.uiowa.edu/distribution/humanfl.html
Seq primer: pYX-5.

FEATURES

Location/Qualifiers

1..739

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/clone="IMAGE:3056889"

/tissue_type="lymph"

/cell_type="germinal center B cells"

/cell_line="MGC85"

/lab_host="DH10B (lTI)"

/clone_lib="NIH MGC 51"

/note="Vector: pYX3-Pac; Site 1: NotI; Site 2: Eco RI;

Constructed from size fractionated cytoplasmic mRNA

(4.4-7.4kb). Directionally cloned. Cells provided by

Louis M. Staudt, Ph.D. Library preparation by Maria de

Fatima Bonaldo, Ph.D. and M. Bento Soares, Ph.D."

ORIGIN

Query Match 12.3%; Score 701.2; DB 14; Length 739;

Best Local Similarity 98.0%; Pred. No. 1.2e-148;

Matches 720; Conservative 0; Mismatches 14; Indels 1; Gaps 1;

QY 2352 GAAGACCCCAAGATCTCATGTTAGTGGAGAGGGTTTCCAACTGAAAGATCTGTA 2411

Db 6 GGAGACCCCAAGATCTCATGTTANAGTGGAGAGGGTTTCCAACTGAAAG-TCTGTA 64

QY 2412 GAGAGTAGCAGTATTTCACTGGTACTGCTATCTGATTTATGGCACTCAGGAAAGTATCTCG 2471

Db 65 GAGAGTAGCAGTATTTCACTGGTACTGCTATCTGATTTATGGCACTCAGGAAAGTATCTCG 124

QY 2472 TTACTGGAGTTAGCACTCTAGGAGGCAAAAACAGAACCAATAATGTTGTGAGTCAG 2531

Db 125 TTACTGGAGTTAGCACTCTAGGAGGCAAAAACAGAACCAATAATGTTGTGAGTCAG 184

QY 2532 TGTCAGAGTATTTGAAACCCCAAGGCACTAATTCATGTTGTTCCAAAGATAATAGAAAT 2591

Db 185 TGTCAGAGTATTTGAAACCCCAAGGCACTAATTCATGTTGTTCCAAAGATAATAGAAAT 244

QY 2592 GACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTACCAAGTCGGGAAACAGC 2651

Db 245 GACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTACCAAGTCGGGAAACAGC 304

QY 2652 ATAGAAATGGAAGAAAGTGAACCTCATGCTCAGTATTTGCAGATACATTTCAAGTTTCA 2711

Db 305 ATAGAAATGGAAGAAAGTGAACCTCATGCTCAGTATTTGCAGATACATTTCAAGTTTCA 364

QY 2712 AAGGCCAGTCAATTTGCTCTGTTTCAATCCAGGAATGAGAGAGGAATGTCACACA 2771

Db 365 AAGGCCAGTCAATTTGCTCTGTTTCAATCCAGGAATGAGAGAGGAATGTCACACA 424

QY 2772 TTCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACCTTTTGAATGTGAA 2831

Db 425 TTCTGCGCCACTCTGGGTCCTTAAAGAAACAAAGTCCAAAAGTCACCTTTTGAATGTGAA 484

QY 2832 CAAAAGGAAGAAATCAAGGAAGAAATGAGTCTAATATCAAGCCCTGTACAGACAGTTAAT 2891

Db 485 CAAAAGGAAGAAATCAAGGAAGAAATGAGTCTAATATCAAGCCCTGTACAGACAGTTAAT 544

QY 2892 ATCACTGAGGCTTCCCTGTTGGTTCAGAAAGTAAGCCAGTTGATTAATGCCAATGT 2951

Db 545 ATCACTGAGGCTTCCCTGTTGGTTCAGAAAGTAAGCCAGTTGATTAATGCCAATGT 604

QY 2952 AGTATCAAGAGGCTCTAGTGTGTTTGTCTATCTCATCTCAGTTTCAGAGGCAACGAACTGGA 3011

Db 605 AGTATCAAGAGGCTCTAGTGTGTTTGTCTATCTCATCTCAGTTTCAGAGGCAACGAACTGGA 664

QY 3012 CTCATTACTCCAAATAACATGGACTTTTACAAACCCCAATATCGTATACCACTTTT 3071

Db 665 CTCATTACTCCAAATAACATGGACTTTTACAAACCCCAATATCGTATACCACTTTT 724

QY 3072 CCCATCAAGTCAATT 3086

Db 725 TCCATCAAGTCAATT 739

RESULT 15

BUI47444

LOCUS

DEFINITION

BUI47444

ACCESSION

BUI47444

VERSION

BUI47444.1

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgabs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LUAM13566 row: 0 column: 13

High quality sequence stop: 695.

FEATURES

source

1..856

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/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6181860"

/sex="male"

/tissue_type="dorsal root ganglia"

/dev_stage="adult, 36 yr"

/lab_host="DH10B"

/clone_lib="Lupski dorsal root ganglion"

/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:

NotI; Site 2: SalI; cDNA made by oligo-dT priming.

Directionally cloned using the following adaptors:

5'-TCGACCCAGGCTCCG-3' and

5'-GACTAGTTCTAGATCGGACGCGCCCT(15)-3'. Size selected >

1 kb for average insert length 1.7 kb. This is a primary

library, non-amplified. Library constructed by Life

Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor

College of Medicine) and is available through Life

Technologies."

ORIGIN

Query Match

Best Local Similarity 97.9%; Pred. No. 6.7e-148;

Matches 762; Conservative 0; Mismatches 5; Indels 11; Gaps 5;

QY 1 AGCTCGCTGAGACTTCCTGGAGCCCGCCAGCCAGCTGTGGGGTTCTCAGATAACTGGGCC 60

Db 82 AGCTCGCTGAGACTTCCTGGAGCCCGCCAGCCAGCTGTGGGGTTCTCAGATAACTGGGCC 140

QY 61 CTTGCGCTCAGGAGGCTTCACCCCTCTGCTCTGGGTAAAGTTCAATTCGAAACAGAAAGAAA 120

Db 141 CTTGCGCTCAGGAGGCTTCACCCCTCTGCTCTGCTCTGCTG-----GTTCAATTCGAAACAGAAAGAAA 194

QY 121 TCGATTTTCTCTCTCTCGGTTGAGAGAGTACAAATGTCATTAATGCTATCGAGAAA 180

Db 195 TCGATTTTCTCTCTCTCGGTTGAGAGAGTACAAATGTCATTAATGCTATCGAGAAA 254

QY 181 TCTTAGAGTGTCTTCATCTGTCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 240

Db 255 TCTTAGAGTGTCTTCATCTGTCTGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC 314

Qy 241 ACATATTTTGCATTTTGCATGCTGAAACTTCTCAACCAAGAAAGGGCCTTTCACAGT 300
Db |||||
Qy 315 ACATATTTTGCATTTTGCATGCTGAAACTTCTCAACCAAGAAAGGGCCTTTCACAGT 374
Db |||||
Qy 301 GTCCTTTAAGTAAGTAATGATATATACCAAAAGAGCCTACAAAGAAAGTAAGAGATTAGTC 360
Db |||||
Qy 375 GTCCTTTAAGTAAGTAATGATATATACCAAAAGAGCCTACAAAGAAAGTAAGAGATTAGTC 434
Db |||||
Qy 361 AACTTGTGTAAGAGCTATTGAAATCAATTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 420
Db |||||
Qy 435 ARCTTGTGTAAGAGCTATTGAAATCAATTGTGCTTTTTCAGCTTGACACAGGTTTGGAGT 494
Db |||||
Qy 421 ATGCAACAGCTATAATTTTGCATAAAAGGAAATAACTCTCTGGAACATCTATAAAGATG 480
Db |||||
Qy 495 ATGCAACAGCTATAATTTTGCATAAAAGGAAATAACTCTCTGGAACATCTATAAAGATG 554
Db |||||
Qy 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 540
Db |||||
Qy 555 AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG 614
Db |||||
Qy 541 AACCCGAAATCCTTCTCTGAGGAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
Db |||||
Qy 615 AACCCGAAATCCTTCTCTGAGGAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 674
Db |||||
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAGAGACGTCTGTCTACATTG 660
Db |||||
Qy 675 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAGAGACGTCTGTCTACATTG 734
Db |||||
Qy 661 AATTGGGATCTGATTTCTTCAAGATACCGTTTAATAGGCAACTTATTGCAAGTGTG- GGA 719
Db |||||
Qy 735 AATTGGGATCTGATTTCTTCAAGATACCGTTTAATAGGCAACTTATTGCAAGTGTGNGGA 794
Db |||||
Qy 720 GATCAAG- AATTGTTACAAATCAACCCCTCAAGGACCAAGGG- -ATGAATCAGTTTGG 774
Db |||||
Qy 795 GATCAAGAAATTGTTACAAATCAACCCCTCAAGGACCAAGGGAAATGAATCAGTTTGG 852
Db |||||

Search completed: June 12, 2004, 06:28:03
Job time : 13209 secs

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Query Match 100.0%; Score 5711; DB 1; Length 5711;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
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DB	1	AGCTCGCTGAGACTTCTCGACCCGCCACAGCTGTGGGGTTCTCAGATACTGGGCC	60						
QY	61	CTGCGCTCAGAGGCTTCACTCTGCTCTGGTAAAGTTCAATGGACAGAGAAA	120						
DB	61	CTGCGCTCAGAGGCTTCACTCTGCTCTGGTAAAGTTCAATGGACAGAGAAA	120						
QY	121	FGGATTTATCTGCTCTCTGCGTTGGAAGAAGTACAAAATGTCATTAATGTCAGAGAAA	180						
DB	121	FGGATTTATCTGCTCTCTGCGTTGGAAGAAGTACAAAATGTCATTAATGTCAGAGAAA	180						
QY	181	TCTAGAGTGTCCATCTGTCTGGAGTTGATCAGGAACTGTCTCCACAAAGTGTGACC	240						
DB	181	TCTAGAGTGTCCATCTGTCTGGAGTTGATCAGGAACTGTCTCTCCAAAGTGTGACC	240						
QY	241	ACATATTTGCAAAATTTGCACTGCTGAACTTCTCAACAGAGAAAGGCGCTTCACT	300						
DB	241	ACATATTTGCAAAATTTGCACTGCTGAACTTCTCAACAGAGAAAGGCGCTTCACT	300						
QY	301	GTCTTTATGAGATGATATTAACCAAGAGGCTTACAGAAAGTACGAGATTAGTC	360						
DB	301	GTCTTTATGAGATGATATTAACCAAGAGGCTTACAGAAAGTACGAGATTAGTC	360						
QY	361	AACCTGTGAGAGCTATTGAAATCATTTGCTCTTTCAGCTTGACACAGGTTGGAGT	420						
DB	361	AACCTGTGAGAGCTATTGAAATCATTTGCTCTTTCAGCTTGACACAGGTTGGAGT	420						
QY	421	ATGCAAAACAGCTATAATTTTGCAGAAAGGAAATAACTCTCTGCAACATCTAAAGATG	480						
DB	421	ATGCAAAACAGCTATAATTTTGCAGAAAGGAAATAACTCTCTGCAACATCTAAAGATG	480						
QY	481	AGTTTCTATCATCAAGATATGGCTACAGAAACGTCGCAAGAGACTTCTACAGAGTG	540						
DB	481	AGTTTCTATCATCAAGATATGGCTACAGAAACGTCGCAAGAGACTTCTACAGAGTG	540						
QY	541	AACCCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACCTCTCTAACCTTGGAA	600						
DB	541	AACCCGAAATCTCTCTGAGGAAACAGCTCTCAGTGTCCAACCTCTCTAACCTTGGAA	600						
QY	601	CTGTGAGACTCTGAGGACAAAGCAGCGGATACAACTCAGGAGCTCTGTCTACATTG	660						
DB	601	CTGTGAGACTCTGAGGACAAAGCAGCGGATACAACTCAGGAGCTCTGTCTACATTG	660						
QY	661	AATTGGGATCTGATTCTTCTGAGATACCGTTAATAGGCACTTATTCAGTGTGGAG	720						
DB	661	AATTGGGATCTGATTCTTCTGAGATACCGTTAATAGGCACTTATTCAGTGTGGAG	720						
QY	721	ATCAAGATTTGTACAAATCACCCCTCAAGGACCAAGGATGAATCAGTTGGATTCTG	780						
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QY	781	CABAAAAGGCTGTGTGGAATTTCTGAGACGATGTAAACAAATCTGAACATCATCAAC	840						
DB	781	CABAAAAGGCTGTGTGGAATTTCTGAGACGATGTAAACAAATCTGAACATCATCAAC	840						
QY	841	CCAGTAAATATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGGCTCCAGAAAAGT	900						
DB	841	CCAGTAAATATGATTTGAAACCACTGAGAGCGTGCAGCTGAGAGGCTCCAGAAAAGT	900						
QY	901	ATCAGGGTGTCTGTTTCAAACTTCCATGTGAGCGATGTGGCAAAATCTCATGCCA	960						
DB	901	ATCAGGGTGTCTGTTTCAAACTTCCATGTGAGCGATGTGGCAAAATCTCATGCCA	960						
QY	961	GCTCATTACAGCTAGAGACAGAGTTTATTTACTCACTAAAGACAGATGAATGTAGAAA	1020						
DB	961	GCTCATTACAGCTAGAGACAGAGTTTATTTACTCACTAAAGACAGATGAATGTAGAAA	1020						
QY	1021	AGGCTGAATTTCTGTAATAAAAGCAACAGCTGTGCTTAGCAAGAGCCAAATACAGAT	1080						
DB	1021	AGGCTGAATTTCTGTAATAAAAGCAACAGCTGTGCTTAGCAAGAGCCAAATACAGAT	1080						
QY	1081	GGGCTGGAAGTAAGAAACATGTATGTAGGCGGACTCCAGCAGCAGAAAAAAGGTAG	1140						
DB	1081	GGGCTGGAAGTAAGAAACATGTATGTAGGCGGACTCCAGCAGCAGAAAAAAGGTAG	1140						
QY	1141	ATCTGAATGTGATCCCTGTGTGAGAGAAAAGTAAGTAAGCAGAAAAATGCCATGCT	1200						
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QY	1201	CAGAGAACTCTAGAGATCTCAAGATGTTCTTGGATAACACTAAATAGAGCATTCAGA	1260						
DB	1201	CAGAGAACTCTAGAGATCTCAAGATGTTCTTGGATAACACTAAATAGAGCATTCAGA	1260						
QY	1261	AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGATGTTAGTGTCTGATGACTCACATGATG	1320						
DB	1261	AAGTTAATGAGTGTGTTTCCAGAAAGTGAATGATGTTAGTGTCTGATGACTCACATGATG	1320						
QY	1321	GGGAGTCTGAATCAAAATGCCCAAAGTAGCTGATGTAATGAGACGTTCTAAATGAGGTAGTG	1380						
DB	1321	GGGAGTCTGAATCAAAATGCCCAAAGTAGCTGATGTAATGAGACGTTCTAAATGAGGTAGTG	1380						
QY	1381	AAATTTCTGCTCTTCTCAGAGAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTTAA	1440						
DB	1381	AAATTTCTGCTCTTCTCAGAGAAATAGACTTACTGGCCAGTGATCTCATGAGGCTTTAA	1440						
QY	1441	TATGTAAAGTGAAGAGTCTCACTCCAAATCAGTAGAGAGTAATATGAAGACAAAATAT	1500						
DB	1441	TATGTAAAGTGAAGAGTCTCACTCCAAATCAGTAGAGAGTAATATGAAGACAAAATAT	1500						
QY	1501	TTGGAAAAACCTATTCGGAAGAGGCAAGCCTCCCACTTAAGCCATGTAACTGAAAATC	1560						
DB	1501	TTGGAAAAACCTATTCGGAAGAGGCAAGCCTCCCACTTAAGCCATGTAACTGAAAATC	1560						
QY	1561	TAATTTATAGGAGCATTTGTTACTGAGCCACAGATAATACAAGAGGTCCTCCCTCAAAATA	1620						
DB	1561	TAATTTATAGGAGCATTTGTTACTGAGCCACAGATAATACAAGAGGTCCTCCCTCAAAATA	1620						
QY	1621	AATTAAGCGTAAAGAGAGCCTACATCAGGCTTCTCATCTGAGAGATTTTATCAAGAAAG	1680						
DB	1621	AATTAAGCGTAAAGAGAGCCTACATCAGGCTTCTCATCTGAGAGATTTTATCAAGAAAG	1680						
QY	1681	CAGATTTGGCGAGTTCAGAGAGCTCTGGAATGATAATACAAGAGCTAACCAACGGAGC	1740						
DB	1681	CAGATTTGGCGAGTTCAGAGAGCTCTGGAATGATAATACAAGAGCTAACCAACGGAGC	1740						
QY	1741	AGAATGGTCAAGTGAATATTTACTAATAGTGTCTATGAGATTAATAAACAAGGTGATT	1800						
DB	1741	AGAATGGTCAAGTGAATATTTACTAATAGTGTCTATGAGATTAATAAACAAGGTGATT	1800						
QY	1801	CTATTCAGAAATGAGAAATCTTAACCAATAGATCACTCGAAGAGAAATCTGCTTCA	1860						
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DB	1921	ACAATTCAAAAGCCTTAAAGAAATAGGCTGAGAGGAGTCTTCTACAGGCAATATTC	1980						
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 20:16:35 ; Search time 356 Seconds
(without alignments)
8902.597 Million cell updates/sec

Title: US-09-734-672A-3

Perfect score: 5711

Sequence: 1 AGCTGCTCAGACTTCCTGG.....TCCCCCAGCCACTACTGA 5711

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 segs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

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- 2: /cgn2.6/prodata/2/ina/5B-COMB.seq:*
- 3: /cgn2.6/prodata/2/ina/6A-COMB.seq:*
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- 6: /cgn2.6/prodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	5711	100.0	5711	3	US-08-825-886-10
3	5711	100.0	5711	3	US-09-074-476-3
4	5709.4	100.0	5711	1	US-08-598-591-1
5	5709.4	100.0	5711	1	US-08-798-691-1
6	5709.4	100.0	5711	3	US-08-825-886-12
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8	5707.8	99.9	5711	4	US-10-022-819-1
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ALIGNMENTS

RESULT 1

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; Sequence 5, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Alvarez, Antonette C.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.
; APPLICANT: Schelter, Denise B.
; APPLICANT: Zeng, Bin
; TITLE OF INVENTION: Coding Sequences of the Human
; TITLE OF INVENTION: BRCA1 Gene
; NUMBER OF SEQUENCES: 72
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ONCORMED
; STREET: 200 Perry Parkway
; CITY: Gaithersburg
; STATE: MD
; COUNTRY: USA
; ZIP: 20877
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent'n Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/798.691
; FILING DATE: 12-Feb-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Thomas Gallegos
; REGISTRATION NUMBER: 32,692
; REFERENCE/DOCKET NUMBER: PA-0054CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-527-2051
; TELEFAX: 301-208-6997
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; ORIGINAL SOURCE:
; ORGANISM: Homo sapiens
; STRAIN: BRCA1
; POSITION IN GENOME:
; CHROMOSOME/SEGMENT: 17

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RESULT 2
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 ; Sequence 5, Application US/08825487A
 ; Patent No. 6048689
 ; GENERAL INFORMATION:
 ; APPLICANT: MUEBLY, Patricia D.
 ; APPLICANT: White, Margie B.
 ; TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENC
 ; NUMBER OF SEQUENCES: 110
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Howrey & Simon
 ; STREET: 1299 Pennsylvania Avenue., N.W.
 ; CITY: Washington,
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20004
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/825,487A
 ; FILING DATE: 28-MAR-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US98/060002
 ; FILING DATE: 26-Mar-1998
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Albert P. Halluin
 ; REGISTRATION NUMBER: 25,227
 ; REFERENCE/DOCKET NUMBER: 05371.0012.999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 650-463-8100
 ; TELEFAX: 650-463-8400
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 5711 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: cDNA
 ; ORGANISM: Homo sapiens
 ; STRAIN: BRCA1

POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-825-487A-5

Query Match 100.0%; Score 5711; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5711; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy	4501	GTGAATACCCCTATAAGCCAGAACTCAGAAAGCCCTTTCTGTGACAAAGTTGAGGTGCTG	4560
Db	4501	GTGNAATACCCCTATAAGCCAGAACTCAGAAAGCCCTTTCTGTGACAAAGTTGAGGTGCTG	4560
Qy	4561	CAGATAGTTCTTACAGTAAAAAATAAGAACACAGAGTGGAAGGTCATGCCCTTCTAAAT	4620
Db	4561	CAGATAGTTCTTACAGTAAAAAATAAGAACACAGAGTGGAAGGTCATGCCCTTCTAAAT	4620
Qy	4621	GCCCATCATTTAGATGATAGTGGTACATGACAGATTGCTCTGGGAGTCTTTCAGAAAGAA	4680
Db	4621	GCCCATCATTTAGATGATAGTGGTACATGACAGATTGCTCTGGGAGTCTTTCAGAAAGAA	4680
Qy	4681	ACTACCCATCTCAAGAGAGCTCATTTAAGTTGTTGATGTGGAGGAGCAACAGCTGGAG	4740
Db	4681	ACTACCCATCTCAAGAGAGCTCATTTAAGTTGTTGATGTGGAGGAGCAACAGCTGGAG	4740
Qy	4741	AGTCTGGGCCACACGATTTGACGGAAACATCTTACTTGCACAGGCCAAGATCTTAGAGGGAA	4800
Db	4741	AGTCTGGGCCACACGATTTGAGGAAACATCTTACTTGCACAGGCCAAGATCTTAGAGGGAA	4800
Qy	4801	CCCTTACTTGGAAATCTGGAATCAGCCCTTCTCTGATGACCCCTGATCTGATCTCTCTG	4860
Db	4801	CCCTTACTTGGAAATCTGGAATCAGCCCTTCTCTGATGACCCCTGATCTGATCTCTCTG	4860
Qy	4861	AAGACAGAGCCCCAGAGTCCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCATTTGA	4920
Db	4861	AAGACAGAGCCCCAGAGTCCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCATTTGA	4920
Qy	4921	AAGTTCCCCAAATTGAAAGTTGCAAGATCTGCCCAGGGTCCAGCTGTGCTCTCTACTCTG	4980
Db	4921	AAGTTCCCCAAATTGAAAGTTGCAAGATCTGCCCAGGGTCCAGCTGTGCTCTCTACTCTG	4980
Qy	4981	ATACGTCTGGGTATAATGCAATGCAAGAAAGTGTGACAGGGAGAGCCAGAAATTGCACAG	5040
Db	4981	ATACGTCTGGGTATAATGCAATGCAAGAAAGTGTGACAGGGAGAGCCAGAAATTGCACAG	5040
Qy	5041	CTTCAACAGAAAGGGTCAACAAAAAGATTCCTCATGTTGTTGTTGCTGTGCTGACCCCGAAG	5100
Db	5041	CTTCAACAGAAAGGGTCAACAAAAAGATTCCTCATGTTGTTGTTGCTGTGCTGACCCCGAAG	5100
Qy	5101	AAATTTATGCTGTGTACAGTTTCCAGAAAAACACCATCTTAACTTAATCTAAATTA	5160
Db	5101	AAATTTATGCTGTGTACAGTTTCCAGAAAAACACCATCTTAACTTAATCTAAATTA	5160
Qy	5161	CTGAAGAGAGACTACTCATGTTGTTATGAAAAACAGATGCTGAGTTTGTGTGTGAACGGACAC	5220
Db	5161	CTGAAGAGAGACTACTCATGTTTATGAAAAACAGATGCTGAGTTTGTGTGTGAACGGACAC	5220
Qy	5221	TGAATAATTTTCTAGGAATTCGGGGAGGAAATGGGTAGTTAGCTATTTTCTGGGTGACCC	5280
Db	5221	TGAATAATTTTCTAGGAATTCGGGGAGGAAATGGGTAGTTAGCTATTTTCTGGGTGACCC	5280
Qy	5281	AGTCTATTAAAGAAAGAAAAATGCTGAATGAGCAATGATTTTGAAGTCAAGAGGAGATGTGG	5340
Db	5281	AGTCTATTAAAGAAAGAAAAATGCTGAATGAGCAATGATTTTGAAGTCAAGAGGAGATGTGG	5340

```

1  RESULT 3
2  US-09-074-476-3
3  ; Sequence 3, Application US/09074476
4  ; Patent No. 6130322
5  ; GENERAL INFORMATION:
6  ; APPLICANT: Murphv, Patricia D.
7  ; APPLICANT: Allen, Antonette C.
8  ; APPLICANT: Alvares, Christopher P.
9  ; APPLICANT: Critz, Brenda S.
10 ; APPLICANT: Olson, Sheri J.
11 ; APPLICANT: Thurber, Denise
12 ; APPLICANT: Zeng, Bin
13 ; TITLE OF INVENTION: Coding Sequences of the Human
14 ; Nucleosome
15 ; NUMBER OF SEQUENCES: 72
16 ; CORRESPONDENCE ADDRESS:
17 ; ADDRESSEE: Howrey & Simon
18 ; STREET: 1299 Pennsylvania Avenue N. W.
19 ; CITY: Washington
20 ; STATE: DC
21 ; COUNTRY: USA
22 ; ZIP: 20004
23 ; COMPUTER READABLE FORM:
24 ; MEDIUM TYPE: Floppy disk
25 ; COMPUTER: IBM PC compatible
26 ; OPERATING SYSTEM: PC-DOS/MS-DOS
27 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
28 ; CURRENT APPLICATION DATA:
29 ; APPLICATION NUMBER: US/09/074,476
30 ; FILING DATE:
31 ; CLASSIFICATION:
32 ; PRIOR APPLICATION DATA:
33 ; APPLICATION NUMBER: 09/074,453
34 ; FILING DATE:
35 ; ATTORNEY/AGENT INFORMATION:
36 ; NAME: Albert P. Halluin
37 ; REGISTRATION NUMBER: 25,227
38 ; REFERENCE/DOCKET NUMBER: 5371.34.US01
39 ; TELECOMMUNICATION INFORMATION:
40 ; TELEPHONE: 650-463-8109
41 ; TELEFAX: 650-463-8400
42 ; INFORMATION FOR SEQ ID NO: 3:
43 ; SEQUENCE CHARACTERISTICS:
44 ; LENGTH: 5711 base pairs

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		TYPE: nucleic acid		Query Match		100.0%; Score 5711; DB 3; Length 5711;	
		STRANDEDNESS: not relevant		Best Local Similarity		100.0%; Pred. No. 0;	
		TOPOLOGY: linear		Matches 5711; Conservative		0; Mismatches 0; Indels 0; Gaps 0;	
		MOLECULE TYPE: cDNA					
		ORIGINAL SOURCE:					
		ORGANISM: Homo sapiens					
		STRAIN: BRCAL (om12)					
		POSITION IN GENOME:					
		CHROMOSOME/SEGMENT: 17					
		MAP POSITION: 17q21					
US-09-074-476-3							
QY	1	AGCTGCGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA	120				
DB	1	AGCTGCGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA	120				
QY	61	CTGCGGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA	120				
DB	61	CTGCGGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAAA	120				
QY	121	TGGAATTTATCTGCTCTTGGCTTTGAAGAAAGTACAAATGTCTAATGCTATGCGAGAAA	180				
DB	121	TGGAATTTATCTGCTCTTGGCTTTGAAGAAAGTACAAATGTCTAATGCTATGCGAGAAA	180				
QY	181	TCTTAGAGTGTCCATCTCTCTGGAGTTGATCAAGGAACCTCTCTCCAAAGTGTGACC	240				
DB	181	TCTTAGAGTGTCCATCTCTCTGGAGTTGATCAAGGAACCTCTCTCCAAAGTGTGACC	240				
QY	241	ACATATTTTGCATTTTTCATCTGCTGAACTTCTCAACCAAGAGAAAGGCGCTTCAACAGT	300				
DB	241	ACATATTTTGCATTTTTCATCTGCTGAACTTCTCAACCAAGAGAAAGGCGCTTCAACAGT	300				
QY	301	GTCTTTTATGTAAGATGATATAACCAAGAGGAGCTTCAAGAAAGTACAGATTTAGTC	360				
DB	301	GTCTTTTATGTAAGATGATATAACCAAGAGGAGCTTCAAGAAAGTACAGATTTAGTC	360				
QY	361	AACTTTTGAAGAGCTTATGAAATCTTGTGCTTTTCAAGAGAGGCGCTTCAACAGT	420				
DB	361	AACTTTTGAAGAGCTTATGAAATCTTGTGCTTTTCAAGAGAGGCGCTTCAACAGT	420				
QY	421	ATGCAACAGCTTATTAATTTTGCATTTTGAAGAAAGTAACTCTCTGAAATCTTAAAGATG	480				
DB	421	ATGCAACAGCTTATTAATTTTGCATTTTGAAGAAAGTAACTCTCTGAAATCTTAAAGATG	480				
QY	481	AACTTTTCTATCTCAAGATGAGCTACAGAAACCGTGGCCTTCAAGAGCTTCTACAGATG	540				
DB	481	AACTTTTCTATCTCAAGATGAGCTACAGAAACCGTGGCCTTCAAGAGCTTCTACAGATG	540				
QY	541	AAACCGAAATCTTCTCTTGCAGGAAACCGAGTCTCAGTGTCCAACTCTCTTAACCTTGGAA	600				
DB	541	AAACCGAAATCTTCTCTTGCAGGAAACCGAGTCTCAGTGTCCAACTCTCTTAACCTTGGAA	600				
QY	601	CTGTGAGAACTCTGAGGACAAAGCGGAGTACAACTTCAAGAGAGCTTGTCTACATTTG	660				
DB	601	CTGTGAGAACTCTGAGGACAAAGCGGAGTACAACTTCAAGAGAGCTTGTCTACATTTG	660				
QY	661	AAATGGGATCTGATCTTCTGAGGATACCGTTTAAAGCAACTTATTCAGTGTGGAG	720				
DB	661	AAATGGGATCTGATCTTCTGAGGATACCGTTTAAAGCAACTTATTCAGTGTGGAG	720				
QY	721	ATCAAGAAATGTTTACAAATCAACCTTCAAGGAAACCGAGGATGAATTCAGTTTGGATCTG	780				
DB	721	ATCAAGAAATGTTTACAAATCAACCTTCAAGGAAACCGAGGATGAATTCAGTTTGGATCTG	780				
QY	781	CAAAAGAGCTCTTGTGAATTTTCTGACAGGATGTAACAATCTGAACTCAATCAAC	840				
DB	781	CAAAAGAGCTCTTGTGAATTTTCTGACAGGATGTAACAATCTGAACTCAATCAAC	840				
QY	841	CCAGTAATGATTTTGAACCAACCTGAGAGAGCGTSCAGCTGAGAGGCTCCAGAAAGT	900				
DB	841	CCAGTAATGATTTTGAACCAACCTGAGAGAGCGTSCAGCTGAGAGGCTCCAGAAAGT	900				
QY	901	ATCAGGCTAGTCTCTGTTTCAAACTTGCATGAGGAGCCATGTGGCAAAAATCTCATGCCA	960				
DB	901	ATCAGGCTAGTCTCTGTTTCAAACTTGCATGAGGAGCCATGTGGCAAAAATCTCATGCCA	960				
QY	961	GCTCATACAGCATGAGAAACAGCAAGTTTATCTACCTAAAGACAGAAATGAATGTAGAAA	1020				
DB	961	GCTCATACAGCATGAGAAACAGCAAGTTTATCTACCTAAAGACAGAAATGAATGTAGAAA	1020				
QY	1021	AGGCTGAATCTGTAATAAAGCAACAGCTGCTTAGCAAGGAGCCCAACATACAGAT	1080				
DB	1021	AGGCTGAATCTGTAATAAAGCAACAGCTGCTTAGCAAGGAGCCCAACATACAGAT	1080				
QY	1081	GGGCTGGAAGTAAGAAACATGTAATGATAGCGGAGCTCCAGCAAGAAAAAGGTAG	1140				
DB	1081	GGGCTGGAAGTAAGAAACATGTAATGATAGCGGAGCTCCAGCAAGAAAAAGGTAG	1140				
QY	1141	ATCTGAATCTGATCCCTCTGTCAGAGAAAGAAATGGAATAGCAGAACTGCCATGCT	1200				
DB	1141	ATCTGAATCTGATCCCTCTGTCAGAGAAAGAAATGGAATAGCAGAACTGCCATGCT	1200				
QY	1201	CAGGAATCTCTAGAGATATCTAAGATGTTCTTGGATAACAATAAGAGAGCTTCAAGA	1260				
DB	1201	CAGGAATCTCTAGAGATATCTAAGATGTTCTTGGATAACAATAAGAGAGCTTCAAGA	1260				
QY	1261	AACTTAATGATGCTGTTTCCAGAGAGTGAATGAGTGTAGGTTCTGATGACTCAGATGATG	1320				
DB	1261	AACTTAATGATGCTGTTTCCAGAGAGTGAATGAGTGTAGGTTCTGATGACTCAGATGATG	1320				
QY	1321	GGGAGTCTGAAATCAAAATGCTCAAGATGCTGATGTTTGGAGCTTCTAAATGAGGTAGATG	1380				
DB	1321	GGGAGTCTGAAATCAAAATGCTCAAGATGCTGATGTTTGGAGCTTCTAAATGAGGTAGATG	1380				
QY	1381	AAATATCTCTGTTTCTCAGAGAAATAGACTTACTTGGCCAGTGTCTCTCATGAGGCTTTAA	1440				
DB	1381	AAATATCTCTGTTTCTCAGAGAAATAGACTTACTTGGCCAGTGTCTCTCATGAGGCTTTAA	1440				
QY	1441	TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATAT	1500				
DB	1441	TATGTAAAGTGAAGAGTTCCTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATAT	1500				
QY	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCTCCCTCCCACTTAAGCCATGTAACTGAAAATC	1560				
DB	1501	TTGGGAAAACCTATCGGAAGAGGCAAGCTCCCTCCCACTTAAGCCATGTAACTGAAAATC	1560				
QY	1561	TAAATATAGGAGCATTTTGTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA	1620				
DB	1561	TAAATATAGGAGCATTTTGTACTGAGCCACAGATAATACAGAGCGTCCCTCACAATA	1620				
QY	1621	AAATTAAGCGGTAAAGAGGAGCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680				
DB	1621	AAATTAAGCGGTAAAGAGGAGCTTACATCAGGCTTCTCATCTGAGGATTTTATCAAGAAAG	1680				
QY	1681	CAGATTTGGCAGTTCAAAGAGCTCTCTGAATGATTAATCATGAGAAATAAAACAAAAGGTGATT	1740				
DB	1681	CAGATTTGGCAGTTCAAAGAGCTCTCTGAATGATTAATCATGAGAAATAAAACAAAAGGTGATT	1740				
QY	1741	AGAATGCTCAAGTGAATGATTAATTAATAGTGTCTCATGAGAAATAAAACAAAAGGTGATT	1800				
DB	1741	AGAATGCTCAAGTGAATGATTAATTAATAGTGTCTCATGAGAAATAAAACAAAAGGTGATT	1800				
QY	1801	CTATTTCAGATGAGAAAAATCTTAAACCAATAGATCACTCGAAAAAGATCTGCTTTCA	1860				
DB	1801	CTATTTCAGATGAGAAAAATCTTAAACCAATAGATCACTCGAAAAAGATCTGCTTTCA	1860				
QY	1861	AAACGAAAGCTGAAACCTTAAGCAGCAGTATTAAGCAATATGGAATCGAATTAATATCC	1920				
DB	1861	AAACGAAAGCTGAAACCTTAAGCAGCAGTATTAAGCAATATGGAATCGAATTAATATCC	1920				
QY	1921	ACAAATTCAGAGCACTTAAAGAAATAGGCTGAGGAGAGTCTTCTTACAGGAGCATATTC	1980				
DB	1921	ACAAATTCAGAGCACTTAAAGAAATAGGCTGAGGAGAGTCTTCTTACAGGAGCATATTC	1980				

TELEFAX: 703-836-2021
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5711 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: not relevant
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:
 ORGANISM: Homo sapiens
 STRAIN: BRCAL
 POSITION IN GENOME:
 CHROMOSOME/SEGMENT: 17
 MAP POSITION: 17q21
 US-08-598-591-1

Query Match 100.0%; Score 5709.4; DB 1; Length 5711;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	AGCTCGCTGAGACTTCTCTGGACCCCGCCAGGCTGTGGGTTCTCAGATAACTGGGCC	60
Dd	1	AGCTCGCTGAGACTTCTCTGGACCCCGCCAGGCTGTGGGTTCTCAGATAACTGGGCC	60
Qy	61	CCTGGCTCAGAGGCTTCACTCTCTCTGGTAAAGTTCAATGGACAGAAAGAA	120
Dd	61	CCTGGCTCAGAGGCTTCACTCTCTCTGGTAAAGTTCAATGGACAGAAAGAA	120
Qy	121	TGGATTATCTGCTCTCTGGGTTGAAGAGTACAAAATGTCAATTAATCTATGAGAAAA	180
Dd	121	TGGATTATCTGCTCTCTGGGTTGAAGAGTACAAAATGTCAATTAATCTATGAGAAAA	180
Qy	181	TCTTAGAGTGTCCATCTGCTGGAGTTGATCAGAGAACTGTCTCCAAAAGTGTGACC	240
Dd	181	TCTTAGAGTGTCCATCTGCTGGAGTTGATCAGAGAACTGTCTCCAAAAGTGTGACC	240
Qy	241	ACATATTTGCAAAATTTTGGCATCTGAACTTCTCAACAGAGAAAGGCTTCAACAGT	300
Dd	241	ACATATTTGCAAAATTTTGGCATCTGAACTTCTCAACAGAGAAAGGCTTCAACAGT	300
Qy	301	GTCTTTATGTAAGATCATATAACCAAAAGAGGCTTCAAGAAAGTACGAGTTAGTC	360
Dd	301	GTCTTTATGTAAGATCATATAACCAAAAGAGGCTTCAAGAAAGTACGAGTTAGTC	360
Qy	361	AACCTGTTGAGAGCTATTGAAATCAATTTGCTTTTCACTTGACACAGCTTGGAGT	420
Dd	361	AACCTGTTGAGAGCTATTGAAATCAATTTGCTTTTCACTTGACACAGCTTGGAGT	420
Qy	421	ATGCAACAGCTATATAATTTGCAAAAGAGGAAATAACTCTCTGAAACATCTAAAGATG	480
Dd	421	ATGCAACAGCTATATAATTTGCAAAAGAGGAAATAACTCTCTGAAACATCTAAAGATG	480
Qy	481	AAGTTTCTATCATCAAGATATGGCTACAGAACCGTGCACAAAGACTTCTACAGATG	540
Dd	481	AAGTTTCTATCATCAAGATATGGCTACAGAACCGTGCACAAAGACTTCTACAGATG	540
Qy	541	AACCCGAAATCTTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCAACCTTGGAA	600
Dd	541	AACCCGAAATCTTCTCTGAGGAAACAGTCTCAGTGTCCAACTCTCAACCTTGGAA	600
Qy	601	CTGTGAGAACTCTGAGGCAAAAGCAGGATACAACTCTCAAAAGAGCTTCTGTACATTTG	660
Dd	601	CTGTGAGAACTCTGAGGCAAAAGCAGGATACAACTCTCAAAAGAGCTTCTGTACATTTG	660
Qy	661	AATTGGGATCTGATTTCTGAGATACCGTTTAAAGGCACTTATTGAGTGTGGAG	720
Dd	661	AATTGGGATCTGATTTCTGAGATACCGTTTAAAGGCACTTATTGAGTGTGGAG	720
Qy	721	ATCAGAAATGTTACAAATACCCCTCAAGGACAGGATGAAATCAATTTGATTTCTG	780
Dd	721	ATCAGAAATGTTACAAATACCCCTCAAGGACAGGATGAAATCAATTTGATTTCTG	780
Qy	781	CAAAAAGGCTGCTTGTGAAATTTCTGAGACGATGTAACAAATCTCAATCATCAAC	840

Db	781	CAAAAAGGCTGCTTGTGAAATTTCTGAGACGATGTAACAAATCTCAATCATCAAC	840
Qy	841	CCAGTAATAATGATTTGAACACCACTGAGAGGCTGAGCTGAGGCTATCCAGAAAAGT	900
Dd	841	CCAGTAATAATGATTTGAACACCACTGAGAGGCTGAGCTGAGGCTATCCAGAAAAGT	900
Qy	901	ATCAGGCTAGTCTGTTTCAAACTTGCATGTGAGCCATGTGGCACAATACTCATGCCA	960
Dd	901	ATCAGGCTAGTCTGTTTCAAACTTGCATGTGAGCCATGTGGCACAATACTCATGCCA	960
Qy	961	GCTCATTACAGCATGAGAACAGCAGTATTATTCTCATTAAAGACAGATGATCTAGAAA	1020
Dd	961	GCTCATTACAGCATGAGAACAGCAGTATTATTCTCATTAAAGACAGATGATCTAGAAA	1020
Qy	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTTAGCAAGGAGCAACATAACAGAT	1080
Dd	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCCTGGCTTTAGCAAGGAGCAACATAACAGAT	1080
Qy	1081	GGGCTGGAAGTAAAGAAACATGTAATGATAGGGGAGCTCCAGACAGAAAAAGGTAG	1140
Dd	1081	GGGCTGGAAGTAAAGAAACATGTAATGATAGGGGAGCTCCAGACAGAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGAATAGCAAGAACTGCCATGCT	1200
Dd	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGAATAGCAAGAACTGCCATGCT	1200
Qy	1201	CAGAGAACTCTAGAGATACCTGGAATGTTCTTGGATTAACACTAAATAGCAGCAATCAGA	1260
Dd	1201	CAGAGAACTCTAGAGATACCTGGAATGTTCTTGGATTAACACTAAATAGCAGCAATCAGA	1260
Qy	1261	AGTTAATGAGTGGTTTCCAGAGGATGATCACTGTTAGGCTCTGATGACTCAGCATGATG	1320
Dd	1261	AGTTAATGAGTGGTTTCCAGAGGATGATCACTGTTAGGCTCTGATGACTCAGCATGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCCAAAGTACTGATGTTTGGACGTTCTAAATCAGCTAGATG	1380
Dd	1321	GGGAGTCTGAATCAAAATGCCAAAGTACTGATGTTTGGACGTTCTAAATCAGCTAGATG	1380
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Dd	1381	AATATTCTGTTCTTCHAGAGAAATAGACTTACTGGCAGTGTCTCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATTAATTAATGAAGACAAATAT	1500
Dd	1441	TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGATTAATTAATGAAGACAAATAT	1500
Qy	1501	TTGGGAAAACCTATCGGAAGAGCAAGCCTCCCAACCTTAAGCCATGTAACCTGAAAATC	1560
Dd	1501	TTGGGAAAACCTATCGGAAGAGCAAGCCTCCCAACCTTAAGCCATGTAACCTGAAAATC	1560
Qy	1561	TAATTATAGGAGCAATTTGTTACTGAGCCACAGATATAACAGAGCGTCCCTCAAAATA	1620
Dd	1561	TAATTATAGGAGCAATTTGTTACTGAGCCACAGATATAACAGAGCGTCCCTCAAAATA	1620
Qy	1621	AATTAAGCCGTAAAGAGACCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG	1680
Dd	1621	AATTAAGCCGTAAAGAGACCTACATCAGGCTTCACTCTGAGGATTTTATCAAGAAAG	1680
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Dd	1681	CAGTTTGGCAGTTCAAAAGACCTCTGAAATGATAATCAGGGAACCTAACCAAGCGGAGC	1740
Qy	1741	AGATGCTCAAGTGATGAATATTACTAATAGTGTCTATGAGAATTAACCAAGGCTGATT	1800
Dd	1741	AGATGCTCAAGTGATGAATATTACTAATAGTGTCTATGAGAATTAACCAAGGCTGATT	1800
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Dd	1801	CTATTGAGATGAGAAAAATCTTAACCCCAATAGATCACTTCGAAAAAGATCTGCTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTTATAGCAGCAGTATAGCAATATGGAATCTGAAATTAATATCC	1920

Db 1861 AAACGAAGCTGAACCTTATAGCAGCAGTATATAGCAATATGGAATCTGAAATTAATATCC 1920
Qy 1921 ACAATTCAAAGCAGCTAAAGAAATAGCTGAGGAGAAAGTCTCTACACAGGATATTC 1980
Db 1921 ACAATTCAAAGCAGCTAAAGAAATAGCTGAGGAGAAAGTCTCTACACAGGATATTC 1980
Qy 1981 ATGCGCTTGAAGTACTAGTACTAGTAAATCTTAAGCCCACTTAATGTACTGAATTCGAAA 2040
Db 1981 ATGCGCTTGAAGTACTAGTACTAGTAAATCTTAAGCCCACTTAATGTACTGAATTCGAAA 2040
Qy 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA 2100
Db 2041 TTGATAGTTGTTCTAGCAGTGAAGAGATAAAGAAAAAAGTACAAACCAATGCCAGTCA 2100
Qy 2101 GGCAAGCAGAAACCTTACAACTCATGAGAGAGTAAAGAACCTTGCACTGAGAGCCAGAGA 2160
Db 2101 GGCAAGCAGAAACCTTACAACTCATGAGAGAGTAAAGAACCTTGCACTGAGAGCCAGAGA 2160
Qy 2161 GTAACAGCCAAATGCAACAGACAAGTAAAGACATGACAGTATCTTCCACAGCTGA 2220
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Qy 2221 AGTTAAACAAATGCACCTGGTCTTTTACTAAGTGTTCAAATACCAAGTGAATCTTAAAGAT 2280
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Qy 2281 TTGTCATCTTAGCCTTCCAGAGAGAGAAAGAGAGAGAACTAGAAACAGTAAAGTGT 2340
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Qy 2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGGTTTGCAAAATG 2400
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Qy 2401 AAGATCTGTAAGAGTAGCAGTATTTTCACTGGTACTGGTACTGATATGGCTCAGG 2460
Db 2401 AAGATCTGTAAGAGTAGCAGTATTTTCACTGGTACTGGTACTGATATGGCTCAGG 2460
Qy 2461 AAGATCTCTGTTACTGGAAGTTAGCACTCTAGGAGAGGCCAAACAGAAACCAATAAAT 2520
Db 2461 AAGATCTCTGTTACTGGAAGTTAGCACTCTAGGAGAGGCCAAACAGAAACCAATAAAT 2520
Qy 2521 GTGTGAGTCAGTGTGCAGCATTTGAAACCCCAAGGAGCTAATTCATGGTTGTTCCAAAG 2580
Db 2521 GTGTGAGTCAGTGTGCAGCATTTGAAACCCCAAGGAGCTAATTCATGGTTGTTCCAAAG 2580
Qy 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640
Db 2581 ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTGGGACATGAAGTTAAACACAGTC 2640
Qy 2641 GGGAAAACAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCGAATAAT 2700
Db 2641 GGGAAAACAAGCATAGAAATGGAAGAAAGTGAATCTGATGCTCAGTATTTGCGAATAAT 2700
Qy 2701 TCAAGGTTTCAAGGCGCAGTCATTTGCTCTGTTTCAATCCAGGAAATCCAGAGAGG 2760
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Qy 2761 AATGTCAACATTTCTCTGCCACTCTGGGCTCTTAAAGAAACAAGTCCAAAGTCACTT 2820
Db 2761 AATGTCAACATTTCTCTGCCACTCTGGGCTCTTAAAGAAACAAGTCCAAAGTCACTT 2820
Qy 2821 TTGAATGTGAACAAAGAGAAATCAAGAAAGAAATGAGTCTTAATATCAAGCTGTAC 2880
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Qy 2881 AGACAGTTTAATATCACTGACGGCTTCTGTTGGTGGTTCAGAAAGATAAGCCAGTTGATA 2940
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Qy 2941 ATGCCAAATAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000
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Qy 3001 ACGAACCTGACCTCATTTACTCCAAATAAACAATGGAATCTTTTACAAAACCCATATCGTATAC 3060
Db 3001 ACGAACCTGACCTCATTTACTCCAAATAAACAATGGAATCTTTTACAAAACCCATATCGTATAC 3060
Qy 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAATCTCTGTAGAGG 3120
Db 3061 CACCACTTTTCCCATCAAGTCAATTTGTTAAACTAAATGTAAGAAATCTCTGTAGAGG 3120
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Qy 3181 GTACAGTAGCACAATTTAGCCGTAATAACAATAGAGAAATGTTTTTAAAGAGGCCAGCT 3240
Db 3181 GTACAGTAGCACAATTTAGCCGTAATAACAATAGAGAAATGTTTTTAAAGAGGCCAGCT 3240
Qy 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGGCTCCAGTATTAAGTAAA 3300
Db 3241 CAAGCAATATTAATGAAGTAGGTTCCAGTACTTAATGAAGTGGGCTCCAGTATTAAGTAAA 3300
Qy 3301 TAGGTTCCAGTGAAGAAACATTCAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTTGA 3360
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Db 3361 ATGCTATGCTTAGATTTAGGAGGTTTGCACCTGAGGCTCTATTAACAAAGTCTTCCCTGGA 3420
Qy 3421 GTAATTTGAAGCATCTCTGAAATTAAGAAACAGAAATATGAAGAGTAGTTTCAGACTGTTA 3480
Db 3421 GTAATTTGAAGCATCTCTGAAATTAAGAAACAGAAATATGAAGAGTAGTTTCAGACTGTTA 3480
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Db 3601 AAGATCTAGTTTGTCTGAAATTAAGAAAGTCTGCTGCTGTTTTAGCAAAAGCG 3660
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Qy 3721 GTTACCGAGAGAGGCGCAAGAAATTAAGAGTCTCTCAGAGAGAACTTATCTAGTAGAGATG 3780
Db 3721 GTTACCGAGAGAGGCGCAAGAAATTAAGAGTCTCTCAGAGAGAACTTATCTAGTAGAGATG 3780
Qy 3781 AAGAGCTTCCCTCTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTTCTCAGT 3840
Db 3781 AAGAGCTTCCCTCTCCAACTGTTTATTTGGTAAAGTAAACAATATACCTTTCTCAGT 3840
Qy 3841 CTACTAGGCATAGCAACCGTTGCTACCGAGTCTGTCTAAGAACACAGAGGAGAAATTTAT 3900
Db 3841 CTACTAGGCATAGCAACCGTTGCTACCGAGTCTGTCTAAGAACACAGAGGAGAAATTTAT 3900
Qy 3901 TATCATTTGAGATAGCTTAATGATCTGAGTAAACAGCTTAATTTGGCAAGGCAATCTC 3960
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Db 3961 AGGAACATCACTTTAGTGGAGAAACAAAATGTTTCTGCTAGCTTGTGTTTCTTCAAGTGCA 4020
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Db 4021 GTGAATTTGGAAGCTTGAATGCAAAATACAAAACCCAGGATCTTCTTCTTGAATGTTCTT 4080

REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: PA-0054CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2051
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: CDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-798-691-1

Query Match 100.0%; Score 5709.4; DB 1; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Db	1	AGCTCGCTGAGACTTCCTGGACCCCGCACACAGGCTGTGGGGTTTCTCAGATPAACTGGGCC	60
Qy	61	CCTCGCTCAGAGGCGCTTACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAA	120
Db	61	CCTCGCTCAGAGGCGCTTACCTCTGCTCTGGGTAAAGTTCAATGGAAACAGAAAGAA	120
Qy	121	TGGATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCATTAATGCTATGAGAA	180
Db	121	TGGATTTATCTGCTCTTCGCGTTGAAGAAGTACAAAATGTCATTAATGCTATGAGAA	180
Qy	181	TCCTAGAGTGCCTATCTGCTGAGTTGATCAAGGACCTGCTCCACAAAGTGTGACC	240
Db	181	TCCTAGAGTGCCTATCTGCTGAGTTGATCAAGGACCTGCTCCACAAAGTGTGACC	240
Qy	241	ACATATTTTGCAAAATTTTGCACTGCTGAACTTCTCAACGAGAAAGAGGCGCTTACAGT	300
Db	241	ACATATTTTGCAAAATTTTGCACTGCTGAACTTCTCAACGAGAAAGAGGCGCTTACAGT	300
Qy	301	GTCCTTTATGTAAGATATATACCAAGAGGCGCTACAGAAAGTACAGATTTAGTC	360
Db	301	GTCCTTTATGTAAGATATATACCAAGAGGCGCTACAGAAAGTACAGATTTAGTC	360
Qy	361	AACCTTTTGAAGAGCTATTGAAATCATTTTGCTTTTTCAGTTTGACACAGGTTTGAGT	420
Db	361	AACCTTTTGAAGAGCTATTGAAATCATTTTGCTTTTTCAGTTTGACACAGGTTTGAGT	420
Qy	421	ATGCAACAGCTATAATTTTGCAGAAAGAGAAATTAATCTCTCTGAAACATCTAAAGATG	480
Db	421	ATGCAACAGCTATAATTTTGCAGAAAGAGAAATTAATCTCTCTGAAACATCTAAAGATG	480
Qy	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Db	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAGACTTCTACAGAGTG	540
Qy	541	AACCGGAAATCTCTTCTTGAGGAAACCACTGTCAGTGTCCATCTCTTAACCTTGAA	600
Db	541	AACCGGAAATCTCTTCTTGAGGAAACCACTGTCAGTGTCCATCTCTTAACCTTGAA	600
Qy	601	CTGTGAGAACTCTGAGGACCAAGCGATACAACTTCAAGACGCTGCTGTACATTTG	660
Db	601	CTGTGAGAACTCTGAGGACCAAGCGATACAACTTCAAGACGCTGCTGTACATTTG	660
Qy	661	AATGGGATCTGATTTCTGAGATACCGTTAATAAGGCACTTATTCAGTGTGGAG	720
Db	661	AATGGGATCTGATTTCTGAGATACCGTTAATAAGGCACTTATTCAGTGTGGAG	720
Qy	721	ATCAAGATTTGTACAAATCACCCCTCAAGGACCGAGGATGAATCAGTTTGATCTG	780

Db	721	ATCAAGATTTGTACAAATCACCCCTCAAGGACCGAGGATGAATCAGTTTGATCTG	780
Qy	781	CAAAAAGGCTGCTTGTGTAATTTCTGAGACGGATGTAACAATATCTGAACATCATCAAC	840
Db	781	CAAAAAGGCTGCTTGTGTAATTTCTGAGACGGATGTAACAATATCTGAACATCATCAAC	840
Qy	841	CCAGTAATATGATTTTGAACACCACTGAGACGGTGCAGCTGAGAGGCTATCCAGAAAGT	900
Db	841	CCAGTAATATGATTTTGAACACCACTGAGACGGTGCAGCTGAGAGGCTATCCAGAAAGT	900
Qy	901	ATCAGGTTAGTTCTGTTTCAAACTTGTCATGTGGAGCCATGTGGCAAAATATCTATGCCA	960
Db	901	ATCAGGTTAGTTCTGTTTCAAACTTGTCATGTGGAGCCATGTGGCAAAATATCTATGCCA	960
Qy	961	GCTCATTACAGCATGAGAACAGCAGTTTATTACTCTACTAAAGACACAAATGAATGAGAAA	1020
Db	961	GCTCATTACAGCATGAGAACAGCAGTTTATTACTCTACTAAAGACACAAATGAATGAGAAA	1020
Qy	1021	AGGCTGAAATTTCTGTAAATAAAGCAACAGCTGGCTTAGCAAGGCCCAACATACAGAT	1080
Db	1021	AGGCTGAAATTTCTGTAAATAAAGCAACAGCTGGCTTAGCAAGGCCCAACATACAGAT	1080
Qy	1081	GGGCTGGAAGTAAAGAACATGTATGATAGCGGACTCCAGCACAGAAAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAAGAACATGTATGATAGCGGACTCCAGCACAGAAAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTCTGTGTGAGAGAAAGAAATGGAATAGCAGAAATGCCCCATGCT	1200
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Qy	1201	CAGAGATCTAGAGATCTAGAGATGTTCTTGGATACACTAAATAGCAGCATTCAGA	1260
Db	1201	CAGAGATCTAGAGATCTAGAGATGTTCTTGGATACACTAAATAGCAGCATTCAGA	1260
Qy	1261	AGGTTAATGAGTGGTTTCCAGAAAGTATGAACTGTTAGGTTCTGATGACTCACATGATG	1320
Db	1261	AGGTTAATGAGTGGTTTCCAGAAAGTATGAACTGTTAGGTTCTGATGACTCACATGATG	1320
Qy	1321	GGAGTCTGAATCAAAATGCCAAAGTATGATGTTTGAACGTTCTAAATAGGTTAGATG	1380
Db	1321	GGAGTCTGAATCAAAATGCCAAAGTATGATGTTTGAACGTTCTAAATAGGTTAGATG	1380
Qy	1381	AATATTCTGTTCTTCAGAGAAATATAGCTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
Db	1381	AATATTCTGTTCTTCAGAGAAATATAGCTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAAGTGAAGAGTTTCACTCCAAATCAGTACAGAGTAAATTTGAAGACAAATAT	1500
Db	1441	TATGTAAAAGTGAAGAGTTTCACTCCAAATCAGTACAGAGTAAATTTGAAGACAAATAT	1500
Qy	1501	TTGGGAAACCTTATCGAAGAGGCGAGCTCCCGAACTTACCCCATGTAACTGAAATC	1560
Db	1501	TTGGGAAACCTTATCGAAGAGGCGAGCTCCCGAACTTACCCCATGTAACTGAAATC	1560
Qy	1561	TAAATATAGAGCATTTGTTTACTGAGCCACAGATAATACAGAGCGTCCCTCACAAATA	1620
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Qy	1621	AATTAAGCGTAAAGGAGACCTACATCAGGCTTCTATCTGAGGATTTTATCAAGAGAG	1680
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Qy	1681	CAGATTGGCAGTTCAAAAGACTCTCTGAAATGATAATCAGGGAACTAACCAACCGGAGC	1740
Db	1681	CAGATTGGCAGTTCAAAAGACTCTCTGAAATGATAATCAGGGAACTAACCAACCGGAGC	1740
Qy	1741	AGAAATGGTCAAGTGATGAATATTAATATAGTGGTCTATGAGATATAAACAAGGTTGATT	1800
Db	1741	AGAAATGGTCAAGTGATGAATATTAATATAGTGGTCTATGAGATATAAACAAGGTTGATT	1800
Qy	1801	CTAATTCAGATGAGAAAAATCCCTTAACCCCAATAGAATCACTCGAAAAAGATCTGCTTCA	1860

Qy	4021	GTGAATTTGGAGAGACTTGACCTGCTGCAAAATCAAAACACCCAGGATCCCTTTCTTGATTTGGTTCCTT	4080
Db	4021	GTGAATTTGGAGAGACTTGACCTGCTGCAAAATCAAAACACCCAGGATCCCTTTCTTGATTTGGTTCCTT	4080
Qy	4081	CCAAACAAATGAGGCATCAGTCTCTGAAAGCCAGGGAGTTGGTCTGTAGTGAACAAGGAATTGG	4140
Db	4081	CCAAACAAATGAGGCATCAGTCTCTGAAAGCCAGGGAGTTGGTCTGTAGTGAACAAGGAATTGG	4140
Qy	4141	TTTCAGATGATGAAGAAAGAGGAAACGGCTTTGGAGAAATAATATCAAGAAAGACAAAGCA	4200
Db	4141	TTTCAGATGATGAAGAAAGAGGAAACGGCTTTGGAGAAATAATATCAAGAAAGACAAAGCA	4200
Qy	4201	TGGATTCAAACTTAGGTGAGACGCATCTCGGTGTGAGAGTGAAGAAACAAGCGTCTCTGAG	4260
Db	4201	TGGATTCAAACTTAGGTGAGACGCATCTCGGTGTGAGAGTGAAGAAACAAGCGTCTCTGAG	4260
Qy	4261	ACTGCTCAGGGCTATCCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC	4320
Db	4261	ACTGCTCAGGGCTATCCCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC	4320
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Db	4321	AACATAACCTGNTAAGCTTCAGCAGGAATGCTGNACTTAGAAGCTGTGTTAGACAGC	4380
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Db	4381	ATGGAGCCAGCCCTTTCAAACAGCTACCCCTTCCATCAAGTGACTCTTCTGCCCCCTTGAGG	4440
Qy	4441	ACCTGCGAAATCCAGAAACAAAGCACATCAGAAAAGCAGTATTAACTTTCAGAAAAGTA	4500
Db	4441	ACCTGCGAAATCCAGAAACAAAGCACATCAGAAAAGCAGTATTAACTTTCAGAAAAGTA	4500
Qy	4501	GTGGAATACCCCTATAAGCCAGAACTCAGAGGCCCTTTCTGCTGCAAGTTTGAAGTGTCTG	4560
Db	4501	GTGGAATACCCCTATAAGCCAGAACTCAGAGGCCCTTTCTGCTGCAAGTTTGAAGTGTCTG	4560
Qy	4561	CAGATAGTTCTTACAGTAAAAATAAGAAACAGAGGTGGAAGGTCAATCCCTTCTAAAT	4620
Db	4561	CAGATAGTTCTTACAGTAAAAATAAGAAACAGAGGTGGAAGGTCAATCCCTTCTAAAT	4620
Qy	4621	GCCCATCATTAGATGATAGTGTGTACATGTCACAGTTGCTCTCTGGGAGTCTTTCAGAAAGAA	4680
Db	4621	GCCCATCATTAGATGATAGTGTGTACATGTCACAGTTGCTCTCTGGGAGTCTTTCAGAAAGAA	4680
Qy	4681	ACTACCCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGGAGGCAACAGCTGGAAG	4740
Db	4681	ACTACCCATCTCAAGAGAGCTCATTAAGTGTGTGATGTGAGGAGGCAACAGCTGGAAG	4740
Qy	4741	AGTCTGGGCCACACGATTTGACGGAAACATCTTACTTTCGCCAAGCAGAGATCAGAGGGA	4800
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Qy	4801	CCCCCTTACTTGGAACTCTGGAATCAGCCCTCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG	4860
Db	4801	CCCCCTTACTTGGAACTCTGGAATCAGCCCTCTTCTCTGATGACCCCTGAAATCTGATCCTTCTG	4860
Qy	4861	AAGACAGAGCCCCAGATGCTAGTCTGTGTGGCAACATACCATCTTCAAACCTCTGCAATTGA	4920
Db	4861	AAGACAGAGCCCCAGATGCTAGTCTGTGTGGCAACATACCATCTTCAAACCTCTGCAATTGA	4920
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Db	4981	ATATCTGCTGGGTATAATTCGAAATGGAAGAAAGTGTGACAGGGAGAAACCCAGAAATTGACAG	5040
Qy	5041	CTTTCACAGGAAGGGTCAACAAAGATGTCCATGGTGGTGTCTGGCCCTGACCCCAAG	5100
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BRSTT.T 6

RESULTS 6
US-08-825-487A-1

US-08-825-48/A-1
Application HS/099354972

; Sequence 1, Application

; Patent No. 6048689

; GENERAL INFORMATION:

; APPLICANT: Murphy, Patricia

APPLICANT: ~~White, Marga B.~~

TITLE OF INVENTION: METHOD

NUMBER OF SEQUENCES: 1

; NUMBER OF SEQUENCES: 110
: CORRESPONDENCE ADDRESS:

; CORRESPONDENCE ADDRESS:
; ADDRESS: HANLEY & SIMON

; ADDRESS: Howrey
COUNTY: 0000 Person

STREET: 1299 Penn

; CITY: Washin:

; STATE: DC

COUNTRY: USA

ZIP: 20004

U.S. GOVERNMENT PRINTING OFFICE: 1969 O - 348-100

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; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk

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; MEDIUM TYPE: FLOPPY DISK
; COMPTON: IBM PC COMPATIBLE

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COMPUTER: IBM PC compatible
OPERATING SYSTEM: DOS/MS DOS

OPERATING SYSTEM: PC-DOS

; SOFTWARE: Patent in F

; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/825,487A

FILING DATE: 28-MAR-1997

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 05371.0012.999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8100
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-825-487A-1

Query Match 100.0%; Score 5709.4; DB 3; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 1 AGCTCGCTGAGACTTCTCGACCCCGCACACAGGCTGTGGGTTTCTCAGATAAATCTGGGCC 60
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Db 4381 ATGGGAGCAGGCTTCTAACAGCTACCTTCCATCATTAAGTGACCTTCTGCCCCCTTGAGG 4440
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Db 4441 ACCTCGGAAATCCAGAACAAAGCACAATCAGAAAAAGCAGTATTAATCTCAGAGAAAGTA 4500
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Db 4501 GTGAATACCTATAGCAGGAGTCCAGAGGCTTCTGCTGACAGTGTGAGGCTGCTG 4560
Qy 4561 CAGATAGTTCTACAGTAAATTAAGAACACAGGAGTGAAGGTCATCCCTCTTAAT 4620
Db 4561 CAGATAGTTCTACAGTAAATTAAGAACACAGGAGTGAAGGTCATCCCTCTTAAT 4620
Qy 4621 GCCCATCATAGATAGTGGTACATGACAGTGTCTGCGAGTCTTCAGATAGAA 4680
Db 4621 GCCCATCATAGATAGTGGTACATGACAGTGTCTGCGAGTCTTCAGATAGAA 4680
Qy 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGGTTGTTGATGTGAGGAGCAACAGCTGGAAG 4740
Db 4681 ACTACCCATCTCAAGAGGAGCTCAATTAAGGTTGTTGATGTGAGGAGCAACAGCTGGAAG 4740
Qy 4741 AGTCTGGGCCACACGATTTGAGGAAACATCTTACCTGCGAAGGCAAGATCTAGAGGAA 4800
Db 4741 AGTCTGGGCCACACGATTTGAGGAAACATCTTACCTGCGAAGGCAAGATCTAGAGGAA 4800
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Db 4801 CCCCTTACCTGGAATCTGGAATCAGCTCTCTCTGATGACCTGATCTGATCTCTCTG 4860
Qy 4861 AAGAAGAGCCCGAGAGTCTGCTGTTGGAACATACCATCTTCAACCTCTGATGAA 4920
Db 4861 AAGAAGAGCCCGAGAGTCTGCTGTTGGAACATACCATCTTCAACCTCTGATGAA 4920
Qy 4921 AAGTTCCTCAATGGAAGTTGAGAAATCTGCCAGGTTCCAGCTGCTGCTCATCTACTG 4980
Db 4921 AAGTTCCTCAATGGAAGTTGAGAAATCTGCCAGGTTCCAGCTGCTGCTCATCTACTG 4980
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Db 4981 ATACTGCTGGGTATTAATGCAATGGAAGAAAGTGTGAGGAGGAGGAGGAGAAATGACAG 5040
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Db 5101 AATTTATGCTGCTGTACAGTTTCCAGAAAACACGACATCATCTTTAACTAAATCTAATTA 5160
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Db 5281 AGTCTATTAAAGAAAAGAAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGGATGTGG 5340
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Db 5341 TCAATGGAAGAAACCAACAAGGTTCCAAAGCGAGCAGAGAAATCCAGGACAGAAAGATCT 5400
Qy 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCCAAACATGCCACAGATCAACTGG 5460
Db 5401 TCAGGGGCTAGAAATCTGTTGCTATGCGGCCCTTCCAAACATGCCACAGATCAACTGG 5460
Qy 5461 AATGATGCTGACAGCTGTGTGCTTCTGTGTGAAAGGAGCTTTCAATTCACCCCTG 5520
Db 5461 AATGATGCTGACAGCTGTGTGCTTCTGTGTGAAAGGAGCTTTCAATTCACCCCTG 5520
Qy 5521 GCACAGTGTCCACCCAAATTTGTTGCTGAGCAGAGTGTGAGAGAGTGGGTGTGGACA 5580
Db 5521 GCACAGTGTCCACCCAAATTTGTTGCTGAGCAGAGTGTGAGAGAGTGGGTGTGGACA 5580
Qy 5581 TCCATGCAATTTGGGCAATGTGTGAGGCACTGTGTGAGCCGAGAGTGGGTGTGGACA 5640
Db 5581 TCCATGCAATTTGGGCAATGTGTGAGGCACTGTGTGAGCCGAGAGTGGGTGTGGACA 5640
Qy 5641 GTGTAGCACTCTACAGTCCAGGAGCTGAGACCTACTGATACCCAGATCCCCACA 5700
Db 5641 GTGTAGCACTCTACAGTCCAGGAGCTGAGACCTACTGATACCCAGATCCCCACA 5700
Qy 5701 GCCACTACTGA 5711
Db 5701 GCCACTACTGA 5711

RESULT 7

US-09-074-476-1

; Sequence 1, Application US/09074476

; Patent No. 6130322

; GENERAL INFORMATION:

; APPLICANT: Murphy, Patricia D.

; APPLICANT: Allen, Antonette C.

; APPLICANT: Alvares, Christopher P.

; APPLICANT: Critz, Brenda S.

; APPLICANT: Olson, Sheri J.

; APPLICANT: Thurber, Denise

; APPLICANT: Zeng, Bin

; TITLE OF INVENTION: Coding Sequences of the Human

; TITLE OF INVENTION: BRCAL Gene

; NUMBER OF SEQUENCES: 72

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Howrey & Simon

; STREET: 1299 Pennsylvania Avenue N. W.

; CITY: Washington

; STATE: DC

; COUNTRY: USA

; ZIP: 20004

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/074.476
 FILING DATE:

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/074.453
 FILING DATE:

ATTORNEY/AGENT INFORMATION:
 NAME: Albert P. Halluin
 REGISTRATION NUMBER: 25,227
 REFERENCE/DOCKET NUMBER: 5371.34.US01

TELEPHONE: 650-463-8109
 TELEFAX: 650-463-8400

INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:

LENGTH: 5711 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: not relevant

TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 ORIGINAL SOURCE:

ORGANISM: Homo sapiens
 STRAIN: BRCAL (omil)
 POSITION IN GENOME:

CHROMOSOME/SEGMENT: 17
 MAP POSITION: 17q21

us-09-074-476-1

Query Match 100.0%; Score 5709.4; DB 3; Length 5711;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy	1	AGCTGCTGAGCTTCCTGGACCCCGACAGGCTGTGGGGTTCCTCAGATAACCTGGGCC	60
Db	1	AGCTGCTGAGCTTCCTGGACCCCGACAGGCTGTGGGGTTCCTCAGATAACCTGGGCC	60
Qy	61	CTGCGGCTCAGAGGCTTCACCCCTCTGCTCTGGGTAAGTTCATTGGAAACAGAAAGAAA	120
Db	61	CTGCGGCTCAGAGGCTTCACCCCTCTGCTCTGGGTAAGTTCATTGGAAACAGAAAGAAA	120
Qy	121	TGGATTATCTGCTCTTGGCTTGAAGAGTACAAATATCTATCTATCTATCTATCTATCT	180
Db	121	TGGATTATCTGCTCTTGGCTTGAAGAGTACAAATATCTATCTATCTATCTATCTATCT	180
Qy	181	TCTTAGAGTGTCCCATCTGCTGAGAGTTCATCAAGCAACCTGTCTCCCAAAAGTGTGACC	240
Db	181	TCTTAGAGTGTCCCATCTGCTGAGAGTTCATCAAGCAACCTGTCTCCCAAAAGTGTGACC	240
Qy	241	ACATATTTTGCAAAATTTTGCATGCTGAAACCTTCTCAACAGAAAGGGGCTTCACAGT	300
Db	241	ACATATTTTGCAAAATTTTGCATGCTGAAACCTTCTCAACAGAAAGGGGCTTCACAGT	300
Qy	301	GTCCCTTATGTAAGATGATATAACCAAGAGAGCTACAGAAAGTACGAGATTAGTC	360
Db	301	GTCCCTTATGTAAGATGATATAACCAAGAGAGCTACAGAAAGTACGAGATTAGTC	360
Qy	361	AACTTTTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTCAACAGGTTGGAGT	420
Db	361	AACTTTTGAAGAGCTATTGAAATCATTTGTGCTTTTTCAGCTTCAACAGGTTGGAGT	420
Qy	421	ATGCAACAGCTATTAATTTTGCAAAAGGAAATTAATCTCTCGAATCTTAAAGATG	480
Db	421	ATGCAACAGCTATTAATTTTGCAAAAGGAAATTAATCTCTCGAATCTTAAAGATG	480
Qy	481	AACTTTTCTATCATCAAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGATG	540
Db	481	AACTTTTCTATCATCAAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGATG	540
Qy	541	AACCGAAATCTCTCTTGGAGGAAACGAGTCTCAGTGTCCAACTCTCTAACCTTGGAA	600
Db	541	AACCGAAATCTCTCTTGGAGGAAACGAGTCTCAGTGTCCAACTCTCTAACCTTGGAA	600

Qy	601	CTGTGAGAACTCTGAGGA	660
Db	601	CTGTGAGAACTCTGAGGA	660
Qy	661	AATTGGGATCTGATTTCTTCTGAAAGTACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG	720
Db	661	AATTGGGATCTGATTTCTTCTGAAAGTACCGTTAATAAGGCAACTTATTGCAAGTGTGGAG	720
Qy	721	ATCAAGAAATTTTACAAATCACCCCTCAAGGAAACGAGGATGAAATCAGTTTGGATCTG	780
Db	721	ATCAAGAAATTTTACAAATCACCCCTCAAGGAAACGAGGATGAAATCAGTTTGGATCTG	780
Qy	781	CAAAAAAGGCTCTTGTGAAATTTTCTGAGACGATGTAAACAAATCTCTGAACATCATCAAC	840
Db	781	CAAAAAAGGCTCTTGTGAAATTTTCTGAGACGATGTAAACAAATCTCTGAACATCATCAAC	840
Qy	841	CCAGTAATATGATTTTGAACCAACCTGAGAGGCTGAGGATGAAATGAAATG	900
Db	841	CCAGTAATATGATTTTGAACCAACCTGAGAGGCTGAGGATGAAATGAAATG	900
Qy	901	ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCTGTGGCACAATACTCATGCCA	960
Db	901	ATCAGGCTAGTCTGTTTCAAACTTGCATGTGGAGCCTGTGGCACAATACTCATGCCA	960
Qy	961	GCTCATTTACAGCATGAGAACAGCAGTTTATTCTCACTAAAGACAGAAATGAAATG	1020
Db	961	GCTCATTTACAGCATGAGAACAGCAGTTTATTCTCACTAAAGACAGAAATGAAATG	1020
Qy	1021	AGGCTGAAATCTGTAATAAAGCAACAGCCTGGCTAGCAAGGAGCCACATAACAGAT	1080
Db	1021	AGGCTGAAATCTGTAATAAAGCAACAGCCTGGCTAGCAAGGAGCCACATAACAGAT	1080
Qy	1081	GGGCTGAACTTAAAGGAAACATGTAATGATAGGGGAGCTCCAGCAGCAAGAAAGGTAG	1140
Db	1081	GGGCTGAACTTAAAGGAAACATGTAATGATAGGGGAGCTCCAGCAGCAAGAAAGGTAG	1140
Qy	1141	ATCTGAAATGCTATCCCTGTGTGAGGAAAGAAAGTGAATAGCAGAAATGCGATGCT	1200
Db	1141	ATCTGAAATGCTATCCCTGTGTGAGGAAAGAAAGTGAATAGCAGAAATGCGATGCT	1200
Qy	1201	CAGAGAACTCTAGAGTACTGAAAGATGTTCTCTTGGATAACACTAAATAGCAGATTCAGA	1260
Db	1201	CAGAGAACTCTAGAGTACTGAAAGATGTTCTCTTGGATAACACTAAATAGCAGATTCAGA	1260
Qy	1261	AAGTAAATGAGTGGTTTTCAGAAAGTATGAACTGTGTAGTGTGATGATCTCATGATG	1320
Db	1261	AAGTAAATGAGTGGTTTTCAGAAAGTATGAACTGTGTAGTGTGATGATCTCATGATG	1320
Qy	1321	GGGAGTCTGAATCAAAATGCAAAAGTATGATGATTTGGAGCTTCTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAATCAAAATGCAAAAGTATGATGATTTGGAGCTTCTAAATGAGGTAGATG	1380
Qy	1381	AATAATCTGGTCTTTCAGAAATATAGACTTACTGGCCAGTGTATCTCATGAGGCTTTAA	1440
Db	1381	AATAATCTGGTCTTTCAGAAATATAGACTTACTGGCCAGTGTATCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCCTCCAAATCAGTGTAGAGTATATATTTGAGACAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCCTCCAAATCAGTGTAGAGTATATATTTGAGACAAATAT	1500
Qy	1501	TTGGGAAAACTTATCGGAAGAGGCAAGCCTCCCAACTTTAAGCCATGTAACTGAAATC	1560
Db	1501	TTGGGAAAACTTATCGGAAGAGGCAAGCCTCCCAACTTTAAGCCATGTAACTGAAATC	1560
Qy	1561	TAAATATAGGAGCATTTTGTATCTGAGCCACAGATATATACAGAGGCTCCCTCACAATA	1620
Db	1561	TAAATATAGGAGCATTTTGTATCTGAGCCACAGATATATACAGAGGCTCCCTCACAATA	1620
Qy	1621	AATTTAAAGCGTAAAGGAGACCTACATCAGGCGCTTCTATCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AATTTAAAGCGTAAAGGAGACCTACATCAGGCGCTTCTATCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTTCAAAAGAGCTCTCTGAAATGATTAATCAGGGAACCTAACCAACGGAGC	1740

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QY 1741 AGAATGGTCAAGTGAATGATATTAATAGTGGTCAAGAGATTAATGAATCAAGAGTGAAT 1800
Db 1741 AGAATGGTCAAGTGAATGATATTAATAGTGGTCAAGAGATTAATGAATCAAGAGTGAAT 1800
QY 1801 CTATTGAGATGAGAAATCTTAACCAATAGATCACTCGAAAAAGAACTCGTTTCA 1860
Db 1801 CTATTGAGATGAGAAATCTTAACCAATAGATCACTCGAAAAAGAACTCGTTTCA 1860
QY 1861 AAAAGAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGGAATCGAAATTAATATCC 1920
Db 1861 AAAAGAGCTGAACCTTAAGCAGCAGTATTAAGCAATATGGAATCGAAATTAATATCC 1920
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Db 1921 ACAATTCAAAAGCAGCTTAAGAGATAGGCTGAGAGGAAGTCTTCTACCAAGCATATTC 1980
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Db 1981 ATGGCTTGAAGTGAATAGTGAATCTTAAGCCCACTTAATTTGTAAGTGAATGCAAA 2040
QY 2041 TTGATAGTGGTCTAGCAGTGAAGATTAAGAAAGAAAGTACAAACCAATGCCAGTCA 2100
Db 2041 TTGATAGTGGTCTAGCAGTGAAGATTAAGAAAGAAAGTACAAACCAATGCCAGTCA 2100
QY 2101 GGCACAGCAGAAACCTCAACTCATGGAAGTAAAGAACTTGCACCTGGAGCCCAAGAGA 2160
Db 2101 GGCACAGCAGAAACCTCAACTCATGGAAGTAAAGAACTTGCACCTGGAGCCCAAGAGA 2160
QY 2161 GTAAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTGAATCTTCCAGAGCTGA 2220
Db 2161 GTAAACAGCCAAATGAACAGCAAGTAAAGACATGACAGTGAATCTTCCAGAGCTGA 2220
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Db 2281 TTGTCAAATCTAGCCTTCCAGAGAGAAAGAGAGAACTAGAAACGTAAAGTGT 2340
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Db 2341 CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGCTTTCGCAACTG 2400
QY 2401 AAAATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTACTGATTAAGCACTCAGG 2460
Db 2401 AAAATCTGTAGAGATGACAGTATTTCACTGGTACCTGGTACTGATTAAGCACTCAGG 2460
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QY 2521 GTGTGAGTCAAGTGCAGCAATTTGAAACCCCAAGGCACTAATTCATGGTGTTCGCAAG 2580
Db 2521 GTGTGAGTCAAGTGCAGCAATTTGAAACCCCAAGGCACTAATTCATGGTGTTCGCAAG 2580
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QY 3421 GTAATTTGAAGCTCTGAAATATAAAGCAAGATATGAAGAGTGTTCAGACTGTTA 3480
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QY 3481 ATACAGATTTCTCTCCATATCTGATTTCAAGTATCTTAGAACAGCTTATGGAGAGTATC 3540
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Db 3841 CTACTAGGCATPAGACCCGTTGCTACCGAGTGTCTGTCTAAGAAACACAGAGAGAAATTTAT 3900


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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
  APPLICATION NUMBER: US/10/022,819
  FILING DATE: 22-Apr-2002
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPLICATION NUMBER: 09/074,452
  FILING DATE: 1998-05-06
ATTORNEY/AGENT INFORMATION:
  NAME: <Unknown>
  REGISTRATION NUMBER: <Unknown>
  REFERENCE/DOCKET NUMBER: 044921-5049-01-US
TELECOMMUNICATION INFORMATION:
  TELEPHONE: 202-739-3000
  TELEFAX: 202-739-3001
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
  LENGTH: 5711 base pairs
  TYPE: nucleic acid
  STRANDEDNESS: single
  TOPOLOGY: linear
  MOLECULE TYPE: DNA (genomic)
  HYPOTHETICAL: NO
  ANTI-SENSE: NO
  FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
  ORGANISM: HOMO SAPIENS
  STRAIN: BRCA1
  HAPLOTYPE: OM14
POSITION IN GENOME:
  CHROMOSOME/SEGMENT: 17
  MAP POSITION: 17q21
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-022-819-1
Query Match          99.9%; Score 5707.8; DB 4; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5709; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 AGCTCGCTGAGACTTCTCGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
DB 1 AGCTCGCTGAGACTTCTCGACCCCGCACAGGCTGTGGGTTTCTCAGATAACTGGGCC 60
QY 61 CTTGGCTCAGAGAGGCTTCAACCTCTGCTCTGGGTTAAAGTTTCATTGGAAACAGAAAGAAA 120
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DB 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACAGAGAAAGGGCTTCCACAGT 300
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DB 481 AAGTTTCTATCATCCAAAGTATGGCTACAGAACCGTGCACAAAGACTTCTACAGAGTG 540
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DB 721 ATCAAGAAATTTTACAAATCAACCCCTCAAGAAACCGGATGAATCAGTTTGGATTTCTG 780
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DB 781 CAAAAGAGGCTGCTTGTGAATTTTCTGAGACGGATGTAACAAATACATGAAATCATCAAC 840
QY 841 CCAGTAAATGATTTGAACCACTCAGAACGCTGAGCTGAGAGCATCCAGAAAAGT 900
DB 841 CCAGTAAATGATTTGAACCACTCAGAACGCTGAGCTGAGAGCATCCAGAAAAGT 900
QY 901 ATCAGGCTAGTCTGTTTCAAACTGATGTGGAGCATATGGGACAAATACATCTATGCCA 960
DB 901 ATCAGGCTAGTCTGTTTCAAACTGATGTGGAGCATATGGGACAAATACATCTATGCCA 960
QY 961 GCTCATTTACAGCATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAATGAATCTAGAAA 1020
DB 961 GCTCATTTACAGCATGAGAAACAGCAGTTTATTACTCACTAAAGACAGAAATGAATCTAGAAA 1020
QY 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGCTTAGAGAGGCAACATTAACAGAT 1080
DB 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGCTTAGAGAGGCAACATTAACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGGAAACATGTAATCATAGGCGAGCTCCAGCACAGAAAAAGGTAG 1140
DB 1081 GGGCTGGAAGTAAAGGAAACATGTAATCATAGGCGAGCTCCAGCACAGAAAAAGGTAG 1140
QY 1141 ATCTGAATGCTGATPCCCTCTGTGAGAGAAAGAAATGGAATPAAGCAAAATCTGCTATGCT 1200
DB 1141 ATCTGAATGCTGATPCCCTCTGTGAGAGAAAGAAATGGAATPAAGCAAAATCTGCTATGCT 1200
QY 1201 CAGAGATCCTAGAGATCTGAGATGTTCTCTTGGATAAACACTAAATAGCAGCATTCAGA 1260
DB 1201 CAGAGATCCTAGAGATCTGAGATGTTCTCTTGGATAAACACTAAATAGCAGCATTCAGA 1260
QY 1261 AAGTTAATGAGTGGTTTTTCCAGAGAGTGAATGAACTGTTAGGTTCTGTAGTCACTCATGATG 1320
DB 1261 AAGTTAATGAGTGGTTTTTCCAGAGAGTGAATGAACTGTTAGGTTCTGTAGTCACTCATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCCAAAGTACTGATGTATTTGGAGCTTCTAAATGAGGTAGTG 1380
DB 1321 GGGAGTCTGAATCAAAATGCCAAAGTACTGATGTATTTGGAGCTTCTAAATGAGGTAGTG 1380
QY 1381 AATATTCTGGTTCTTCAGAGAAATAGACTTATCTGGCGCAGTGAATCTCATGAGGCTTTAA 1440
DB 1381 AATATTCTGGTTCTTCAGAGAAATAGACTTATCTGGCGCAGTGAATCTCATGAGGCTTTAA 1440
QY 1441 TATCTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTATGAGAGCAAAATAT 1500
DB 1441 TATCTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTATGAGAGCAAAATAT 1500
QY 1501 TTGGGAAACCTATTCGGAAGAGCAAGCCTCCCAACTTAAAGCCATCTTAATCTGAAATC 1560
DB 1501 TTGGGAAACCTATTCGGAAGAGCAAGCCTCCCAACTTAAAGCCATCTTAATCTGAAATC 1560
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Qy	1561	TAAATATAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAAATA	1620
Db	1561	TAAATATAGGAGCATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCCACAAATA	1620
Qy	1621	AAATTAAGCGTAAAGAGAGACCTACATCAGCGCTTTCATCTCTGAGGATTTTATCAAGAAAG	1680
Db	1621	AAATTAAGCGTAAAGAGAGACCTACATCAGCGCTTTCATCTCTGAGGATTTTATCAAGAAAG	1680
Qy	1681	CAGATTTGGCAGTTCAAAAGACTCTGGAATGATATAATCAGGGAACCTAACCAACGGAGC	1740
Db	1681	CAGATTTGGCAGTTCAAAAGACTCTGGAATGATATAATCAGGGAACCTAACCAACGGAGC	1740
Qy	1741	AGAAATGGTCAAGTGAATATTAATAATAGTGGTCAATGAGAAATTAATAAAGGATTT	1800
Db	1741	AGAAATGGTCAAGTGAATATTAATAATAGTGGTCAATGAGAAATTAATAAAGGATTT	1800
Qy	1801	CTAATTCAGATGAGAAAATCTTAACCCATAGAAATCACTGAAAGAAATCTGCTTTCA	1860
Db	1801	CTAATTCAGATGAGAAAATCTTAACCCATAGAAATCACTGAAAGAAATCTGCTTTCA	1860
Qy	1861	AAACGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATCTCGAATTAATATCC	1920
Db	1861	AAACGAAAGCTGAACCTATAAGCAGCAGTATAAGCAATATGGAATCTCGAATTAATATCC	1920
Qy	1921	ACAAATTCAAAAGCACCTAAAAGAAATAGCTGAGGAGGAAGTCTTTACCAAGGCATATTC	1980
Db	1921	ACAAATTCAAAAGCACCTAAAAGAAATAGCTGAGGAGGAAGTCTTTACCAAGGCATATTC	1980
Qy	1981	ATGCGCTTGAATAGTGTGCTAGCAATCTAAGCCACCTAAATGTACTGAAATGCAAA	2040
Db	1981	ATGCGCTTGAATAGTGTGCTAGCAATCTAAGCCACCTAAATGTACTGAAATGCAAA	2040
Qy	2041	TTGATAGTGTGTTAGTGTGAGAGATTAAGAAAAGATGACAAATGCGAGTCA	2100
Db	2041	TTGATAGTGTGTTAGTGTGAGAGATTAAGAAAAGATGACAAATGCGAGTCA	2100
Qy	2101	GGCAGAGAGAACTTACATCTATGAGAGTAAAGAACCTGCAACTGAGCCAGAGAGA	2160
Db	2101	GGCAGAGAGAACTTACATCTATGAGAGTAAAGAACCTGCAACTGAGCCAGAGAGA	2160
Qy	2161	GTAACAAGCCAAATGAACAGACAGTAAAGACATGACAGTGATATCTTTCCAGAGCTGA	2220
Db	2161	GTAACAAGCCAAATGAACAGACAGTAAAGACATGACAGTGATATCTTTCCAGAGCTGA	2220
Qy	2221	AGTTAAACAATGCACTGGTCTTTTCTAAGTGTTCATATACAGTGAATTAAGAAAT	2280
Db	2221	AGTTAAACAATGCACTGGTCTTTTCTAAGTGTTCATATACAGTGAATTAAGAAAT	2280
Qy	2281	TTGTCAATCCTAGCTTCCAGAGAGAAAAGAGAGAAAAGAGAGAACTAGAAAAGTGT	2340
Db	2281	TTGTCAATCCTAGCTTCCAGAGAGAAAAGAGAGAAAAGAGAGAACTAGAAAAGTGT	2340
Qy	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCAAACTG	2400
Db	2341	CTAATAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGCAAACTG	2400
Qy	2401	AAAGATCTGTACAGAGTAGCAGTATTTCACTGCTGACCTGGTACTGATTTGGCACTCAGG	2460
Db	2401	AAAGATCTGTACAGAGTAGCAGTATTTCACTGCTGACCTGGTACTGATTTGGCACTCAGG	2460
Qy	2461	AAAGATCTGTGCTGAGAGTTAGCACTCTAGGGAAGGCAAAAACAGAACTAAT	2520
Db	2461	AAAGATCTGTGCTGAGAGTTAGCACTCTAGGGAAGGCAAAAACAGAACTAAT	2520
Qy	2521	GTGAGTGTGCTGAGAGTTAGCACTCTAGGGAAGGCAAAAACAGAACTAAT	2580
Db	2521	GTGAGTGTGCTGAGAGTTAGCACTCTAGGGAAGGCAAAAACAGAACTAAT	2580
Qy	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCACTC	2640
Db	2581	ATAATAGAAATGACACAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAACCACTC	2640

Qy	2641	GGGAAACAAGCATAGAAAATGGAAAGAGTGAATCTGATCTCAGTATTTGCGAATACAT	2700
Db	2641	GGGAAACAAGCATAGAAAATGGAAAGAGTGAATCTGATCTCAGTATTTGCGAATACAT	2700
Qy	2701	TCAGAGTTTCAAGCCGAGTCAATTTGCTCTGTTTCAAAATCCAGGAAATGCAAGAGG	2760
Db	2701	TCAGAGTTTCAAGCCGAGTCAATTTGCTCTGTTTCAAAATCCAGGAAATGCAAGAGG	2760
Qy	2761	AATGTCAACATTTCTCTGCCCCTCTGGGCTCTTAAAGAAAACAAGTCCAAAAGTCACTT	2820
Db	2761	AATGTCAACATTTCTCTGCCCCTCTGGGCTCTTAAAGAAAACAAGTCCAAAAGTCACTT	2820
Qy	2821	TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC	2880
Db	2821	TTGAATGTGAACAAAAGGAGAAATCAAGGAAAGATGAGTCTAATATCAAGCCTGTAC	2880
Qy	2881	AGACAGTTAATATACATCTGAGGCTTTCTGTTGTTGCTCAGAAAGATAGCCAGTTGATA	2940
Db	2881	AGACAGTTAATATACATCTGAGGCTTTCTGTTGTTGCTCAGAAAGATAGCCAGTTGATA	2940
Qy	2941	ATGCCAAAATGTATATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941	ATGCCAAAATGTATATCAAAAGGAGGCTCTAGGTTTGTCTATCATCTCAGTTCAGAGGCA	3000
Qy	3001	ACGAAATCTGAGCTCATTTACTCCAAAATAAACAATGGAATTTTACAAAACCCATATCGTATAC	3060
Db	3001	ACGAAATCTGAGCTCATTTACTCCAAAATAAACAATGGAATTTTACAAAACCCATATCGTATAC	3060
Qy	3061	CACACATTTTCCCATCAAGTCAATTTGTTAAATCTAATATGAAAGAAATCTGCTAGAGG	3120
Db	3061	CACACATTTTCCCATCAAGTCAATTTGTTAAATCTAATATGAAAGAAATCTGCTAGAGG	3120
Qy	3121	AAACATTTGAGGAGCAATTCATCTGCAAGAGAGAAATGGGAAATGAGAAATCTTCCAA	3180
Db	3121	AAACATTTGAGGAGCAATTCATCTGCAAGAGAGAAATGGGAAATGAGAAATCTTCCAA	3180
Qy	3181	GTACAGTGAGCACAATTTAGCCGTAAATCAATAGAGAAAAATGTTTTAAAGAGCCAGCT	3240
Db	3181	GTACAGTGAGCACAATTTAGCCGTAAATCAATAGAGAAAAATGTTTTAAAGAGCCAGCT	3240
Qy	3241	CAGCATAATTAATGAGTGTGTTTCCAGTACTAATGAGTGGCTCCAGTATTAATCAAA	3300
Db	3241	CAGCATAATTAATGAGTGTGTTTCCAGTACTAATGAGTGGCTCCAGTATTAATCAAA	3300
Qy	3301	TAGTTCACAGTGTGAGAAACATTTCAAGCAGAACTAGGTAGAGAAACAGAGGCGCAAAATGA	3360
Db	3301	TAGTTCACAGTGTGAGAAACATTTCAAGCAGAACTAGGTAGAGAAACAGAGGCGCAAAATGA	3360
Qy	3361	ATGCTATCTGTAGTTAGGAGGTTTSCAAGCTGAGGCTTATTAACAAAGTCTTCTCGAA	3420
Db	3361	ATGCTATCTGTAGTTAGGAGGTTTSCAAGCTGAGGCTTATTAACAAAGTCTTCTCGAA	3420
Qy	3421	GTAATTCGAAGCATCTGAAATAAAAAGCAAGAAATAGGAAGTAGTTTCAAGCTGTTA	3480
Db	3421	GTAATTCGAAGCATCTGAAATAAAAAGCAAGAAATAGGAAGTAGTTTCAAGCTGTTA	3480
Qy	3481	ATACAGATTTCTCTCATATCTGATTTCAATATTTAGACAGCCTATGGAGTAGTC	3540
Db	3481	ATACAGATTTCTCTCATATCTGATTTCAATATTTAGACAGCCTATGGAGTAGTC	3540
Qy	3541	ATGCATCTCAGGTTTGTCTGAGACACTCATGACCTGTTTAGATGATGCGTGAATAAGG	3600
Db	3541	ATGCATCTCAGGTTTGTCTGAGACACTCATGACCTGTTTAGATGATGCGTGAATAAGG	3600
Qy	3601	AAGTACTAGTTTGTGAAAATGACATTAAGGAAAGTCTGCTGTTTTTGTAGCAAAAAGCG	3660
Db	3601	AAGTACTAGTTTGTGAAAATGACATTAAGGAAAGTCTGCTGTTTTTGTAGCAAAAAGCG	3660
Qy	3661	TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTTCCCATACACATTTGCTCAGG	3720
Db	3661	TCCAGAGAGGAGCTTAGCAGGAGTCTAGCCCTTTTCCCATACACATTTGCTCAGG	3720
Qy	3721	GTTAACCAAGAGGCGGCCAAGAAATTAGAGTCTCTCAGAAAGAGAACTTATCTAGTGGAGT	3780

3721 GTTACCGAGAGGGGCCAAGAAATTAGAGTCTCAGAAGAGAACTTATCTAGTGAGGATG 3780
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3781 AAGAGCTTCCCTGCTTCCAAACCTTGTATTTGGTAAAGTAAACAAATATACCTTCTCAGT 3840
3841 CTACTAGGCATAGCAACCGTGTCTACCGAGTGTCTCTAAGAAACACAGAGGAGAAATTTAT 3900
3841 CTACTAGGCATAGCAACCGTGTCTACCGAGTGTCTCTAAGAAACACAGAGGAGAAATTTAT 3900
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3901 TATCATTTGAGATAGCTTTAAATGATCTGAGTAAACAGGATATATTTGGCAAGGATCTC 3960
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4021 GTGAATTTGGAAGCTTGTGATCTGCAAAATACAAACACCCAGATCTTCTTGTGATTTGCTT 4080
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4081 CCACAAATGAGGATCTGATCTGCAAAATACAAACACCCAGATCTTCTTGTGATTTGCTT 4140
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4201 TGGATTTCAACTAGTGAAGAGGATCTGAGTGAAGAGGATCTGAGTGAAGAGGATCTGAGG 4260
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4261 ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCACTCAGCAGAGGGATACCATGC 4320
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4321 AACATTAACCTGATTAAGCTTCCAGAGGAAATGGCTGAACTAGAGCTGTGTAGAACAGC 4380
4321 AACATTAACCTGATTAAGCTTCCAGAGGAAATGGCTGAACTAGAGCTGTGTAGAACAGC 4380
4381 ATGGAGGAGGAGCTTCTAACAGCTACCTTCCATCATTAAGTGAATCTCTCTGAGGAGG 4440
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4441 ACTGCGAAATCCAGAACAAAGCAATCAGAAAGAGGAGTATTAACCTTCAAGAAAGTA 4500
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4561 CAGATAGTTCTACCAAGTAAATAAAGAACCAAGGAGTGAAGGTCATCCCTCTTCTAAAT 4620
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4621 GCCCATCATAGATAGTGGTATGATGCAAGTGTCTGAGGAGTCTTCAGATAGAA 4680
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4681 ACTTACCCATCTCAAGAGGAGCTCATTAAGTGTGTGATGTGAGGAGCAACAGCTGGAG 4740
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4741 AGTCTGGGCAACAGATTTGAGGAAACATCTTACTTGGCAAGGAGGATCTAGAGGAA 4800
4741 AGTCTGGGCAACAGATTTGAGGAAACATCTTACTTGGCAAGGAGGATCTAGAGGAA 4800
4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTCTCTGATGACCTGATCTGATCTGATCTG 4860

4801 CCCCTTACCTGGAATCTGGAATCAGGCTCTTCTCTGATGAGCCCTGGAATCTGATCTCTG 4860
4861 AAGACAGAGCCCCAGAGCTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCAATGA 4920
4861 AAGACAGAGCCCCAGAGCTCAGCTCGTGTGGCAACATACCATCTTCAACCTCTGCAATGA 4920
4921 AAGTTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGGTCAGCTGCTGCTCACTACTG 4980
4921 AAGTTCCCAATTTGAAAGTTGCAAGATCTGCCAGAGGTCAGCTGCTGCTCACTACTG 4980
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4981 ATACTGCTGGGTATTAATGCAATGGAAGAGTGTGAGCAGGAGGAGGAGGAGGAGGAG 5040
5041 CTTCAACAGAGAGGCTCAACAAAGAAATGTCATGCTGGTGTCTGGCTGACCCAGAG 5100
5041 CTTCAACAGAGAGGCTCAACAAAGAAATGTCATGCTGGTGTCTGGCTGACCCAGAG 5100
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5161 CTGAAGAGAGCTACTCATGTTTATGAAACAGATGCTGAGTTTGTGTGAGGAGGAGGAG 5220
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5221 TGAATATTTTCTAGAGATTCGCGAGGAGAAATGCGGTAGTTAGCTATTTCTGGGTGACCC 5280
5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGGAGATGAG 5340
5281 AGTCTATTAAAGAAAGAAATGCTGAATGAGCATGATTTTGAAGTCAAGAGGAGATGAG 5340
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5341 TCAATGAGAGAACCAACAGGTCCTAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5400
5401 TCAGGGGCTAGAAATCTGCTGATGCGGCTTCAACCAATGCGGCTTCAACCAATGCGGCT 5460
5401 TCAGGGGCTAGAAATCTGCTGATGCGGCTTCAACCAATGCGGCTTCAACCAATGCGGCT 5460
5461 AATGATGAGTACAGCTGTGTGCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5520
5461 AATGATGAGTACAGCTGTGTGCTTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGG 5520
5521 GCAGAGTGTCCACCAATTTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5580
5521 GCAGAGTGTCCACCAATTTGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5580
5581 TCCATGCAATTTGGCAGATGTTGAGGCACTGTGCTGAGGAGGAGGAGGAGGAGGAGGAG 5640
5581 TCCATGCAATTTGGCAGATGTTGAGGCACTGTGCTGAGGAGGAGGAGGAGGAGGAGGAG 5640
5641 GTGTAGCACTCTACAGTGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5700
5641 GTGTAGCACTCTACAGTGTCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 5700
5701 GCCACTACTGA 5711
5701 GCCACTACTGA 5711

RESULT 9
US-08-798-691-3
; Sequence 3, Application US/08798691
; Patent No. 5750400
; GENERAL INFORMATION:
; APPLICANT: Murphy, Patricia D.
; APPLICANT: Allen, Antonette C.
; APPLICANT: Alvares, Christopher P.
; APPLICANT: Critz, Brenda S.
; APPLICANT: Olson, Sheri J.

APPLICANT: Schelter, Denise B.
APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
TITLE OF INVENTION: BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESSEE: ONCORMED
STREET: 200 Perry Parkway
CITY: Gaithersburg
STATE: MD
COUNTRY: USA
ZIP: 20877
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/798,691
FILING DATE: 12-Feb-97
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Thomas Gallegos
REGISTRATION NUMBER: 32,692
REFERENCE/DOCKET NUMBER: PA-0054CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-527-2051
TELEFAX: 301-208-6997
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCA1
POSITION IN GENOME: 17
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-798-691-3

Query Match 99.9%; Score 5703; DB 1; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY	1	AGCTGCTGAGACTTCCTGACCCCGCACAGGCTGTGGGGTTCTCAGATAACTGGGCC	60
DB	1	AGCTGCTGAGACTTCCTGACCCCGCACAGGCTGTGGGGTTCTCAGATAACTGGGCC	60
QY	61	CTTGCGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTTCATTTGGAACAGAAAGAAA	120
DB	61	CTTGCGCTCAGAGGCTTCAACCTCTGCTCTGGGTAAAGTTTCATTTGGAACAGAAAGAAA	120
QY	121	TGATTTATCTGCTCTTCGGGTGAAGAGTACAAATGCTAATTAATGCTATGCAAGAAA	180
DB	121	TGATTTATCTGCTCTTCGGGTGAAGAGTACAAATGCTAATTAATGCTATGCAAGAAA	180
QY	181	TCTTAGAGTGTCCCATCTCTCTGAGTTGATCAAGGAACCTGTCTCCAAAGTGTGACC	240
DB	181	TCTTAGAGTGTCCCATCTCTCTGAGTTGATCAAGGAACCTGTCTCCAAAGTGTGACC	240
QY	241	ACATATTTGCAATTTTCGATCTGAAACTTCTCAACAGAGAAAGGGCTTCACAGT	300
DB	241	ACATATTTGCAATTTTCGATCTGAAACTTCTCAACAGAGAAAGGGCTTCACAGT	300
QY	301	GTCTTTATGTAAGATGATATAACCAAGAGGAGCTCAAGAAAGTACAGATTAGTC	360
DB	301	GTCTTTATGTAAGATGATATAACCAAGAGGAGCTCAAGAAAGTACAGATTAGTC	360
QY	361	AACTTGTGAAGAGCTATTGAAAATCATTTGTGCTTTTCAGCTTGACACAGGTTGGAGT	420
DB		AACTTGTGAAGAGCTATTGAAAATCATTTGTGCTTTTCAGCTTGACACAGGTTGGAGT	420

DB	361	AACTTGTGAAGAGCTATTGAAAATCATTTGTGCTTTTCAGCTTGACACAGGTTGGAGT	420
QY	421	ATCCAAACAGCTATAATTTTGGCAAAAAGAAAATACTCTCTGTAACATCTTAAAGATG	480
DB	421	ATCCAAACAGCTATAATTTTGGCAAAAAGAAAATACTCTCTGTAACATCTTAAAGATG	480
QY	481	AACTTGTATCATCCAAAGTATGGGCTACAGAAACGTCGCAAAAGACTTCTACAGAGTG	540
DB	481	AACTTGTATCATCCAAAGTATGGGCTACAGAAACGTCGCAAAAGACTTCTACAGAGTG	540
QY	541	AACCCGAAAATCCTTCTTGCGAGAAACCAAGTCTCAGTGTCCAACTCTCTTAACTCTGGAA	600
DB	541	AACCCGAAAATCCTTCTTGCGAGAAACCAAGTCTCAGTGTCCAACTCTCTTAACTCTGGAA	600
QY	601	CTGTGAACTCTGAGGACAAACAGCGATACAACTCTCAAAAGAGCTGTCTACATTTG	660
DB	601	CTGTGAACTCTGAGGACAAACAGCGATACAACTCTCAAAAGAGCTGTCTACATTTG	660
QY	661	AATGGGATCTGATTTCTTGAAGTACCGTTAATAAGCAACTTATTCAGTGTGGAG	720
DB	661	AATGGGATCTGATTTCTTGAAGTACCGTTAATAAGCAACTTATTCAGTGTGGAG	720
QY	721	ATCAAGAAATTTTACAAATCAACCCCTCAGGAAACCGGATGAATCAGTTTGTGATCTG	780
DB	721	ATCAAGAAATTTTACAAATCAACCCCTCAGGAAACCGGATGAATCAGTTTGTGATCTG	780
QY	781	CAAAAAGAGCTGTCTTGAAGTACCGTTAATAAGCAACTTATTCAGTGTGGAG	840
DB	781	CAAAAAGAGCTGTCTTGAAGTACCGTTAATAAGCAACTTATTCAGTGTGGAG	840
QY	841	CCAGTAAATGATTTGAACACCACTGAGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT	900
DB	841	CCAGTAAATGATTTGAACACCACTGAGAGAGCGTGCAGCTGAGAGGATCCAGAAAGT	900
QY	901	ATCAGGGTAGTTCTGTTTCAAACTTGCATCTGGAGCCATGTGGCAAAATCTCATGCCA	960
DB	901	ATCAGGGTAGTTCTGTTTCAAACTTGCATCTGGAGCCATGTGGCAAAATCTCATGCCA	960
QY	961	GCTCATTACAGATGAGAAACAGAGTTTATTTACTCCTAAAGACAGAAATGATAGAAA	1020
DB	961	GCTCATTACAGATGAGAAACAGAGTTTATTTACTCCTAAAGACAGAAATGATAGAAA	1020
QY	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCTGCTTTAGCAAGAGGCAACATCAACAGAT	1080
DB	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCTGCTTTAGCAAGAGGCAACATCAACAGAT	1080
QY	1081	GGGCTGGAAGTAAAGAAACATGTAAATCATAGGCGATCTCCAGACAGAAAGAGTAG	1140
DB	1081	GGGCTGGAAGTAAAGAAACATGTAAATCATAGGCGATCTCCAGACAGAAAGAGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGAATAGCAAGAACTGCATGCT	1200
DB	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAGAAATGGAATAGCAAGAACTGCATGCT	1200
QY	1201	CAGAGATCTCTAGAGATATCTGAAGATGTCTCTGGATAACACTAAATAGCAGCAATTG	1260
DB	1201	CAGAGATCTCTAGAGATATCTGAAGATGTCTCTGGATAACACTAAATAGCAGCAATTG	1260
QY	1261	AAGTTAATGATGTGTTTTCAGAAAGTATGAACTGTAGTTCTGATGCTCAGCATGATG	1320
DB	1261	AAGTTAATGATGTGTTTTCAGAAAGTATGAACTGTAGTTCTGATGCTCAGCATGATG	1320
QY	1321	GGGAGTCTGAATCAATAGCCAAAGTAGCTGATGTATTGGAGCTTCTAAATGAGGTAGATG	1380
DB	1321	GGGAGTCTGAATCAATAGCCAAAGTAGCTGATGTATTGGAGCTTCTAAATGAGGTAGATG	1380
QY	1381	AATATCTGTGTTCTCAGAGAAATATAGCTTATGCGCCAGTGATCTCTCATGAGGCTTTAA	1440
DB	1381	AATATCTGTGTTCTCAGAGAAATATAGCTTATGCGCCAGTGATCTCTCATGAGGCTTTAA	1440
QY	1441	TATCTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATAT	1500
DB	1441	TATCTAAAGTGAAGAGTTTCACTCCAAATCAGTAGAGAGTAAATATTGAAGACAAAATAT	1500

[illegible]

APPLICANT: White, Marga B.
TITLE OF INVENTION: METHODS FOR IDENTIFYING VARIATIONS IN POLYNUCLEOTIDE SEQUENCE
NUMBER OF SEQUENCES: 110
CORRESPONDENCE ADDRESS:
ADDRESSEE: Howrey & Simon
STREET: 1299 Pennsylvania Avenue., N.W.
CITY: Washington,
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,487A
FILING DATE: 28-Mar-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US98/060002
FILING DATE: 26-Mar-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 05371.0012.999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8100
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
STRAIN: BRCAL
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21
US-08-825-487A-3

Query Match 99.9%; Score 5703; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 1 AGCTGCTGAGACTTCTGAGACCCCGACAGGCTGTGGGGTTCTCAGATAAATGGGCC 60
Db 1 AGCTGCTGAGACTTCTGAGACCCCGACAGGCTGTGGGGTTCTCAGATAAATGGGCC 60
Qy 61 CTGGGCTCAGAGGCGCTTACCCCTCTGCTGGGTAAGTTCAATGGAAACAGAAAGAA 120
Db 61 CTGGGCTCAGAGGCGCTTACCCCTCTGCTGGGTAAGTTCAATGGAAACAGAAAGAA 120
Qy 121 TGGATTATCTGCTCTTCGGTGTGAAGAGTACAAATGTCTAATGCTATGACAGAAA 180
Db 121 TGGATTATCTGCTCTTCGGTGTGAAGAGTACAAATGTCTAATGCTATGACAGAAA 180
Qy 181 TCTTAGAGTGTCCCATCTGCTGAGAGTTGATCAAGAAACCTGTCTCCACAAAGTGTACC 240
Db 181 TCTTAGAGTGTCCCATCTGCTGAGAGTTGATCAAGAAACCTGTCTCCACAAAGTGTACC 240
Qy 241 ACATATTTGCAATTTTGCATGCTGAACTTCTCAACACAGAAAGGCGCTTACACAGT 300
Db 241 ACATATTTGCAATTTTGCATGCTGAACTTCTCAACACAGAAAGGCGCTTACACAGT 300
Qy 301 GTCTTTATGTAAGATGATATAACCAAAAGAGGCTTACAAAGAGTACGAGATTAGTC 360
Db 301 GTCTTTATGTAAGATGATATAACCAAAAGAGGCTTACAAAGAGTACGAGATTAGTC 360

Qy 361 AACTTGTGTGAAGAGCTATTGAAAATCATTTGTGCTTTTCAGCTTGCACACAGGTTTGAGT 420
Db 361 AACTTGTGTGAAGAGCTATTGAAAATCATTTGTGCTTTTCAGCTTGCACACAGGTTTGAGT 420
Qy 421 ATGCAACACAGCTATAATTTTGCAGAAAGGAAAATTAACCTCTCTGAGACATCTAAAGATG 480
Db 421 ATGCAACACAGCTATAATTTTGCAGAAAGGAAAATTAACCTCTCTGAGACATCTAAAGATG 480
Qy 481 AAGTTTCTATCATCTCAAAAGTATGGGTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540
Db 481 AAGTTTCTATCATCTCAAAAGTATGGGTACAGAAACCGTGCAGAAAGACTTCTACAGAGTG 540
Qy 541 AACCCGAAATCTCTCTCTGAGAAACAGTCTCAGTGTCTCAGTGTCCAACTCTCTAACTTGGAA 600
Db 541 AACCCGAAATCTCTCTCTGAGAAACAGTCTCAGTGTCTCAGTGTCCAACTCTCTAACTTGGAA 600
Qy 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTGTCTTACATTG 660
Db 601 CTGTGAGAACTCTGAGGACAAAGCAGCGGATACAACTCAAAAGAGCTGTCTTACATTG 660
Qy 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCACTGTGGAG 720
Db 661 AATTGGGATCTGATTCTTCTGAAGATACCGTTAATAAGGCAACTTATTGCACTGTGGAG 720
Qy 721 ATCAAGAAATGTTTACAAATCAACCCCTCAGGAAACAGGATGAATTCAGTTTGTGATTCTG 780
Db 721 ATCAAGAAATGTTTACAAATCAACCCCTCAGGAAACAGGATGAATTCAGTTTGTGATTCTG 780
Qy 781 CAAAAAGGCTGCTGTGTAATTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840
Db 781 CAAAAAGGCTGCTGTGTAATTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 840
Qy 841 CCAGTAATATGATTGAAACACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAGT 900
Db 841 CCAGTAATATGATTGAAACACCACTGAGAAAGCGTGCAGCTGAGAGGATCCAGAAAGT 900
Qy 901 ATCAGGCTGCTGCTGTGTAATTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 960
Db 901 ATCAGGCTGCTGCTGTGTAATTTCTGAGACGGATGTAAACAAATCTGAAACATCATCAAC 960
Qy 961 GCTCATTTACAGATGAGAAACAGAGTTTATTAATCTAAAGAGTGTAAAGTGTGAGAA 1020
Db 961 GCTCATTTACAGATGAGAAACAGAGTTTATTAATCTAAAGAGTGTAAAGTGTGAGAA 1020
Qy 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1080
Db 1021 AGGCTGAATTTCTGTAATAAAGCAACAGCTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGT 1080
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Db 1141 ATCTGAATGCTGATCCCTCTGTGAGAGAAAGATGGAATGGAATGGAATGGAATGGAATGGA 1200
Qy 1201 CAGAGATCTCTAGAGATCTCTGAGAGTGTCTCTTGGATTAACACTAAATAGCAGATTCAGA 1260
Db 1201 CAGAGATCTCTAGAGATCTCTGAGAGTGTCTCTTGGATTAACACTAAATAGCAGATTCAGA 1260
Qy 1261 AAGTTAATGAGTGTGTTTCCAGAGTGTGAACTGTGTTAGTGTCTGATGATCACTGATG 1320
Db 1261 AAGTTAATGAGTGTGTTTCCAGAGTGTGAACTGTGTTAGTGTCTGATGATCACTGATG 1320
Qy 1321 GGGAGTCTGAATCAAAATGCAAAAGTGTGATGTTTGGAGTGTCTTAAATGAGTGTAGT 1380
Db 1321 GGGAGTCTGAATCAAAATGCAAAAGTGTGATGTTTGGAGTGTCTTAAATGAGTGTAGT 1380
Qy 1381 AATATCTGTTCTCTCAGAGAAATAGACTTACCTGCGCAGTGTCTCTCATGAGGCTTTAA 1440
Db 1381 AATATCTGTTCTCTCAGAGAAATAGACTTACCTGCGCAGTGTCTCTCATGAGGCTTTAA 1440
Qy 1441 TATGTAAAGTGAAGAGTTTCACTCCAAATCAGTGTAGAGTGTAAATTTTGAAGACAAATAT 1500

1441 TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATTTGAAGCAAAATAT 1500
1501 TTGGAAAACCTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAATCTGAATAATC 1560
1501 TTGGAAAACCTATCGGAAGAGGCAAGCCTCCCAACTTAAGCCATGTAATCTGAATAATC 1560
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1621 AATTAAAGCGTAAAGAGGACCTACATCAGGCGCTTCACTCCCTGAGGATTTTATCAAGAAAG 1680
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1681 CAGATTTGGCGAGTTCAAAAGACTCCTGAAATGATTAATACAGGAACTAACCAAGCGAGC 1740
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1741 AGAATGGTCAAGTGAATGATTAATCAATAGTGGTCAATGAGAAATAAAACAAAAGGTGATT 1800
1801 CTATTCAGATGAGGAAAATCCTTAACCAATAGATCACTCGAAGAAAGAAATCTGCTTCA 1860
1801 CTATTCAGATGAGGAAAATCCTTAACCAATAGATCACTCGAAGAAAGAAATCTGCTTCA 1860
1861 AAACGAAAGCTGAACCTATAAGACGAGTAAAGCAATATGGAATCTCGAAATTAATATCC 1920
1861 AAACGAAAGCTGAACCTATAAGACGAGTAAAGCAATATGGAATCTCGAAATTAATATCC 1920
1921 ACAATTAAGACCTAAAGAAATAGCTCAGGAGGAGTCTTCTACAGGCAATATTC 1980
1921 ACAATTAAGACCTAAAGAAATAGCTCAGGAGGAGTCTTCTACAGGCAATATTC 1980
1981 ATGCGCTTGAATAGTACAGTGAATTAAGCCCACTAATTTGTAAGTGAATTCGAA 2040
1981 ATGCGCTTGAATAGTACAGTGAATTAAGCCCACTAATTTGTAAGTGAATTCGAA 2040
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2041 TTGATAGTGTCTAGAGTGAGAGATTAAGAAAATAAGATCAACCAATGCGAGTCA 2100
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2161 GTAACAGCCAAATCAACAGACAAGTAAAGACAATGACAGTGATATCTTCCAGAGCTGA 2220
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2221 AGTTAAAGATGCACTGCTGTTCTTTTCTAAGTGTTCATTAAGTCAATCCAGTCAATTAAGAAAT 2280
2281 TTGTCAAATCTAGCCTTCCAGAGAGAAAAGAGAGAACTAGAAACAGTAAAGTGT 2340
2281 TTGTCAAATCTAGCCTTCCAGAGAGAAAAGAGAGAACTAGAAACAGTAAAGTGT 2340
2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGGCAACTG 2400
2341 CTAATTAATGCTGAAGACCCCAAGATCTCATGTTAAGTGGAGAAAGGTTTGGCAACTG 2400
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2401 AAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2460
2461 AAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2520
2461 AAAGATCTGTAGAGAGTACAGTATTTCACTGGTACCTGGTACTGATTTATGGCACTCAGG 2520
2521 GTGTAGTGCAGTGCAGCATTTGAAACCCCAAGGAGTAAATTCATGTTGTTCCAAAG 2580

2521 GTGTAGTGCAGTGCAGCATTTGAAACCCCAAGGAGCTAATTTCAATGTTGTTCCAAAG 2580
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2581 ATATTAAGATGACACAGAGGCTTTAAAGTATCCATTTGGACATGAAGTTAAACCAAGTC 2640
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2941 ATGCCAAATGTAGTATCAAGGAGGCTTTAGGTTTGTCTATCATCTCAGTTCAGAGGCA 3000
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3001 ACCAACTGAGCTCATTTACTCCAAATTAACATCGACTTTTACAAAACCCATATCGTATAC 3060
3061 CACACATTTTCCCATCAAGTCAATTTGTTAAACATAAATGTAAGAAAATCTCTAGAGG 3120
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3121 AAAACCTTGGAGGACATTCATCTCACTGCAAGGAAATGGGAAATGAGAACTCCAA 3180
3121 AAAACCTTGGAGGACATTCATCTCACTGCAAGGAAATGGGAAATGAGAACTCCAA 3180
3181 GTAAGTGCACAAATTAGCCGTAATCAATTAAGAGAAAATGTTTAAAGAGGAGCAGCT 3240
3181 GTAAGTGCACAAATTAGCCGTAATCAATTAAGAGAAAATGTTTAAAGAGGAGCAGCT 3240
3241 CAAGCAATATTAATGAGTAGGTTCCAGTACTAATGAAGTGGCTCCAGTATTAATGAAA 3300
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3301 TAGGTTCCAGTGTGAAAAATCAAGCAGAACTAGGTAGAAAACAGAGGCGCCAAAATTTGA 3360
3301 TAGGTTCCAGTGTGAAAAATCAAGCAGAACTAGGTAGAAAACAGAGGCGCCAAAATTTGA 3360
3361 ATGCTATGCTTAGATTAGGAGGTTTCCAGCTGAGTCTATTAACAAAGTCTTCTCGGAA 3420
3361 ATGCTATGCTTAGATTAGGAGGTTTCCAGCTGAGTCTATTAACAAAGTCTTCTCGGAA 3420
3421 GTAATTTCAAGCATCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTTA 3480
3421 GTAATTTCAAGCATCTGAAATTAAGAAAGCAAGATATGAAGAGTAGTTCAGACTGTTA 3480
3481 ATCAGATTTCTCTCCATCTGATTTTCAGATAATTCAGTAACAGCCCTATGGGAGTAGTC 3540
3481 ATCAGATTTCTCTCCATCTGATTTTCAGATAATTCAGTAACAGCCCTATGGGAGTAGTC 3540
3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGCTGTTAGATGATGGTGAATTAAGG 3600
3541 ATGCATCTCAGGTTTGTCTGAGACACCTGATGCTGTTAGATGATGGTGAATTAAGG 3600
3601 AAGATACTAGTTCCTGCAAAATGACATTAAGGAAAGTCTCTGCTGTTTGTAGCAAAAGCG 3660
3601 AAGATACTAGTTCCTGCAAAATGACATTAAGGAAAGTCTCTGCTGTTTGTAGCAAAAGCG 3660

GENERAL INFORMATION:
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APPLICANT: Alvares, Christopher P.
APPLICANT: Critz, Shendi S.
APPLICANT: Olson, Sheri J.
APPLICANT: Thurber, Denise
APPLICANT: Zeng, Bin
TITLE OF INVENTION: Coding Sequences of the Human
TITLE OF INVENTION: BRCA1 Gene
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
ADDRESS: Howrey & Simon
STREET: 1299 Pennsylvania Avenue N. W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/074,476
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/074,453
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Albert P. Halluin
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 5371.34.US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-463-8109
TELEFAX: 650-463-8400
INFORMATION FOR SEQ ID NO. 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 5711 base pairs
TYPE: nucleic acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: cDNA
ORGANISM: Homo sapiens
STRAIN: BRCA1 (om13)
POSITION IN GENOME:
CHROMOSOME/SEGMENT: 17
MAP POSITION: 17q21

US-09-074-476-5

Query Match 99.9%; Score 5703; DB 3; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5706; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy	1	AGCTCGCTGAGACTTCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAAAGTGGGCC	60
Db	1	AGCTCGCTGAGACTTCTGGACCCCGCACAGGCTGTGGGTTTCTCAGATAAAGTGGGCC	60
Qy	61	CTGGGCTCAGAGGCTTCAACCTCTGCTGGTAAAGTTTCATTGGAACAGAAAGAAA	120
Db	61	CTGGGCTCAGAGGCTTCAACCTCTGCTGGTAAAGTTTCATTGGAACAGAAAGAAA	120
Qy	121	TGGATTTATCTGCTCTGCGTTGAGAGAGTACAAAATGTCATTAACTATGAGAAA	180
Db	121	TGGATTTATCTGCTCTGCGTTGAGAGAGTACAAAATGTCATTAACTATGAGAAA	180
Qy	181	TCTTAGAGTGCCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCAAAGTGTGACC	240
Db	181	TCTTAGAGTGCCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCAAAGTGTGACC	240
Qy	241	ACATATTTGCAAAATTTTTCATGCTGAAACTTCTCAACAGAGAAAGGCGCTTCACAGT	300

Db	241	ACATATTTGCAAAATTTTTCATGCTGAAACTTCTCAACAGAGAAAGGCGCTTCACAGT	300
Qy	301	GTCTTTATGTAAGATGATATAACCAAGAGGCTTACAGAAAGTACAGATTTAGTC	360
Db	301	GTCTTTATGTAAGATGATATAACCAAGAGGCTTACAGAAAGTACAGATTTAGTC	360
Qy	361	AACCTTGTGAAGAGCTATTGAAATCATTTTGTGCTTTTCAGCTTGCACACAGGTTGAGT	420
Db	361	AACCTTGTGAAGAGCTATTGAAATCATTTTGTGCTTTTCAGCTTGCACACAGGTTGAGT	420
Qy	421	ATGCAAAACAGCTATATTTTGCAAAAGAGAAATTAACCTCTCTGAACATCTAAAGATG	480
Db	421	ATGCAAAACAGCTATATTTTGCAAAAGAGAAATTAACCTCTCTGAACATCTAAAGATG	480
Qy	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG	540
Db	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCCAAAAGACTTCTACAGAGTG	540
Qy	541	AACCCGAAATCCCTTCTTCAGAGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTTGGAA	600
Db	541	AACCCGAAATCCCTTCTTCAGAGAAACCAAGTCTCAGTGTCCAACTCTCTAACTTTGGAA	600
Qy	601	CTGTGAGAACTCTCAGGACAAAGCAGCGATACAACTCAAAAGAGCTGTGTCTACATTG	660
Db	601	CTGTGAGAACTCTCAGGACAAAGCAGCGATACAACTCAAAAGAGCTGTGTCTACATTG	660
Qy	661	AATGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTCAGTGTGGAG	720
Db	661	AATGGGATCTGATTTCTTGAAGATACCGTTAATAAGGCAACTTATTCAGTGTGGAG	720
Qy	721	ATCAGAAATTTTACAAATCAACCCCTCAGGACCAAGGATGAAATCAGTTTGGATTCTG	780
Db	721	ATCAGAAATTTTACAAATCAACCCCTCAGGACCAAGGATGAAATCAGTTTGGATTCTG	780
Qy	781	CAAAAAGGCTGCTTGTGAAATTTTCTGAGACCGATGTAAACAAATCTGAACATCATCAAC	840
Db	781	CAAAAAGGCTGCTTGTGAAATTTTCTGAGACCGATGTAAACAAATCTGAACATCATCAAC	840
Qy	841	CCAGTAAATGATTTGAAACACCACTGAGAGGCTGCGAGCTGAGAGGCTCCAGAAAGT	900
Db	841	CCAGTAAATGATTTGAAACACCACTGAGAGGCTGCGAGCTGAGAGGCTCCAGAAAGT	900
Qy	901	ATCAGGCTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA	960
Db	901	ATCAGGCTAGTTCTGTTTCAAACTTGCATGTGGAGCCATGTGGCACAATACTCATGCCA	960
Qy	961	GCTCATTACAGCATGAGACAGAGTTTATCTACTTAAGACAGATGATGATGTAGAAA	1020
Db	961	GCTCATTACAGCATGAGACAGAGTTTATCTACTTAAGACAGATGATGATGTAGAAA	1020
Qy	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCGCTGGCTTAGCAAGGAGCCAACTAACAGAT	1080
Db	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCGCTGGCTTAGCAAGGAGCCAACTAACAGAT	1080
Qy	1081	GGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCAGCAAAAAAGGTAG	1140
Db	1081	GGCTGGAAGTAAAGAAACATGTAATGATAGGCGGACTCCAGCAGCAAAAAAGGTAG	1140
Qy	1141	ATCTGATGCTGATCCCTCTGTGTGAGAAAGAAATGGAATTAAGCAGAAATCTGCATGCT	1200
Db	1141	ATCTGATGCTGATCCCTCTGTGTGAGAAAGAAATGGAATTAAGCAGAAATCTGCATGCT	1200
Qy	1201	CAGAGAACTCTAGAGATGATGAAAGATGTTCTCTTGGATAACACTAAATAGCAGCATTCAGA	1260
Db	1201	CAGAGAACTCTAGAGATGATGAAAGATGTTCTCTTGGATAACACTAAATAGCAGCATTCAGA	1260
Qy	1261	AAGTTAATGATGGTTTCCAGAAAGTATCAACTGTGTAGGTTCTGTGATCTCAGATGATG	1320
Db	1261	AAGTTAATGATGGTTTCCAGAAAGTATCAACTGTGTAGGTTCTGTGATCTCAGATGATG	1320
Qy	1321	GGGAGTCTGAAATCAAAATGCGAAAGTATGATGATTTTGGACGTTCTAAATGAGGTAGATG	1380

Db 1321 GGGAGTCTGAATCAATGCCAAAGTAGCTGATGTATTCGACGTTCTAAATGAGGTAGATG 1380
Qy 1381 AATATTCCTGGTCTTCACAGAAATAGACTTACTGGCCAGTGATCCCTCATGAGGCTTTAA 1440
Db 1381 AATATTCCTGGTCTTCACAGAAATAGACTTACTGGCCAGTGATCCCTCATGAGGCTTTAA 1440
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Qy 1561 TAAATATAGGAGCACTTGTACTGAGCCACAGATAATACAAGAGGTCCTCCCTCAAAATA 1620
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Qy 1681 CAGATTTGGCAGTTCACAAAGAGCTCTGAAATGATAAATCAGGGAAGTAACTCAACAGGAGC 1740
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Qy 1801 CTATTCAGAAATGAGAAATCCTTAACCAATAGAAATCACTCGAAAGAGAAATCTGCTTTCA 1860
Db 1801 CTATTCAGAAATGAGAAATCCTTAACCAATAGAAATCACTCGAAAGAGAAATCTGCTTTCA 1860
Qy 1861 AAAAGAGAGTGAACCTATAAGCAGCAGTATAAGCAATATGGAATTAATAATATCC 1920
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Qy 1921 ACAATTCAGAGCCTAAAAGAGATAGCTGAGGAGAGTCTTCTACAGGCAATATTC 1980
Db 1921 ACAATTCAGAGCCTAAAAGAGATAGCTGAGGAGAGTCTTCTACAGGCAATATTC 1980
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Db 1981 ATGCGCTTGAATAGTAGTAGTGAATAATCTAAGCCCACTTAATGTAAGTGAATGCAAA 2040
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Qy 2101 GGCAAGCAGAACTCAACTCACTGGAAGTAAAGAACCTGCACTGAGGCCAAGAGA 2160
Db 2101 GGCAAGCAGAACTCAACTCACTGGAAGTAAAGAACCTGCACTGAGGCCAAGAGA 2160
Qy 2161 GTAAAGCCCAATGAACAGACCAAGTAAAGACATGACAGTGTATCTTCCAGAGCTGA 2220
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Db 2221 AGTTAAAGTGCACCTGGTCTTTTACTAGTGTCTCAATACAGTGAATCTTAAGAAAT 2280
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Db 2461 AAAGTATCTCTGTACTGGAAGTTAGCACTCTAGGAAGGCAAAAACAGAACCCAAATAAAT 2520
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Db 2521 GTGTGAGTCAAGTGTGAGCAATTTGAAAAACCCCAAGGGACTAATTCATGTTGTTTCCAAAG 2580
Qy 2581 ATAATAGAAATGACACAGAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640
Db 2581 ATAATAGAAATGACACAGAGAGGCTTTAAGTATCCATTTGGGACATGAAGTTAAACCAAGTC 2640
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5701 GCCCATCTACTGA 5711

Db 5701 GCCACTACTGA 5711

RESULT 12
US-08-658-322-1
; Sequence 1, Application US/08658322
; Patent No. 5869245
; GENERAL INFORMATION:
; APPLICANT: Yeung, Anthony T.
; TITLE OF INVENTION: Mismatch Endonuclease And Its Use in
; TITLE OF INVENTION: Identifying Mutations in Targeted Polynucleotide Strands
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dunn, Dorfman, Herrell and Skillman, P.C.
; STREET: 1601 Market Street, Suite 720
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103-2307
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,322
; FILING DATE: 05-JUN-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hagan, Patrick J.
; REGISTRATION NUMBER: 27,643
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 563-4100
; TELEFAX: (215) 563-4044
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5711 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: not relevant
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO

US-08-658-322-1

Query Match 99.8%; Score 5701.4; DB 2; Length 5711;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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5701 GCCCACTACTGA 5711

RESULT 13
US-08-603-753D-1
; Sequence 1, Application US/08603753D
; Patent No. 5891857

GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID L.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: SZABO, CSILLA I.
APPLICANT: JETTON, THOMAS L.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARLES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
STREET: BOULEVARD
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/603,753D
FILING DATE: 20 FEB 1996
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995
ATTORNEY/AGENT INFORMATION:
NAME: ARLES A. TAYLOR, JR.
REGISTRATION NUMBER: 39,395
REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5712
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: ductal carcinoma in situ, invasive
CELL TYPE: breast cancer and normal breast tissue
CELL LINE: not derived from a cell line
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA1
LOCATION: GenBank accession no. U14680
IDENTIFICATION METHOD: microscopically directed
IDENTIFICATION METHOD: sampling and nuclease protection assay
OTHER INFORMATION: gene encoding BRCA1 protein
PUBLICATION INFORMATION:

AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 1:

US-08-603-753D-1

Query Match 99.9%; Score 5701.4; DB 2; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
Qy 1 AGCTCGCTGAGACTTCCTGACCCGCCGACAGGCTGTGGGGTTTCTCAGATAAAGTGGCC 60
Db 1 AGCTCGCTGAGACTTCCTGACCCGCCGACAGGCTGTGGGGTTTCTCAGATAAAGTGGCC 60
Qy 61 CTTGCGCTCAGAGGCTTCACCTCTGCTCTGGGTAAGTTTATTGGACACAGAAA 120
Db 61 CTTGCGCTCAGAGGCTTCACCTCTGCTCTGGGTAAGTTTATTGGACACAGAAA 120
Qy 121 TGGATTTATCTGCTCTCGGGTTGAAGAAGTACAAAATGTCATTATGCTATCAGAAA 180
Db 121 TGGATTTATCTGCTCTCGGGTTGAAGAAGTACAAAATGTCATTATGCTATCAGAAA 180
Qy 181 TCTTAGAGTCTCCATCTGTCTGGAGTTGATCAAGAAACCTGTCTCCAAAGTGTGACC 240
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Db 241 ACATATTTTGCATAATTTGTCATGCTGAAACTCTCAACAGAGAAAGGCGCTTCCAGT 300
Qy 301 GTCTTTATCTAAGAAATGATATAACCAAGAGGCTTACAAAGAAAGTACAGATTTAGTC 360
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Qy 361 AACTGTTGAAGAGCTATTGAAATCATTTGCTTTTTCAGCTTGACACAGGTTTGAGT 420
Db 361 AACTGTTGAAGAGCTATTGAAATCATTTGCTTTTTCAGCTTGACACAGGTTTGAGT 420
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Db 421 ATGCAAAACAGCTATAATTTTGCATAAAGAAATAACTCTCTGCAACATCTTAAAGATG 480
Qy 481 AGTTTCTATCATCAAGATATGGGCTCAGAGAACCGTCCAAAGACTTCTACAGATG 540
Db 481 AGTTTCTATCATCAAGATATGGGCTCAGAGAACCGTCCAAAGACTTCTACAGATG 540
Qy 541 AACCCGAAATCTTCTTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
Db 541 AACCCGAAATCTTCTTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
Qy 601 CTGTGAGAACTCTGAGAGCAAAAGCAGGATACAACTCAAGAGAGTCTGTACATTG 660
Db 601 CTGTGAGAACTCTGAGAGCAAAAGCAGGATACAACTCAAGAGAGTCTGTGTACATTG 660
Qy 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGTGGAG 720
Db 661 AATTGGGATCTGATTTCTTGAAGATACCGTTAATAGGCAACTTATTGCAAGTGTGGAG 720
Qy 721 ATCAAGAAATTTTACAAATCACCCCTCAAGAAACCGGATGAAATCAGTTTGATTTCTG 780
Db 721 ATCAAGAAATTTTACAAATCACCCCTCAAGAAACCGGATGAAATCAGTTTGATTTCTG 780
Qy 781 CAAAAGAGGCTCTGTTGAAATTTTCTGAGAGCGGATGTACAAATCTGACATCATCAAC 840
Db 781 CAAAAGAGGCTCTGTTGAAATTTTCTGAGAGCGGATGTACAAATCTGACATCATCAAC 840
Qy 841 CCAGTAATATGATTTTGAACACCACTGAGAGCGGCTGAGAGAGGATCCAGAAAGT 900
Db 841 CCAGTAATATGATTTTGAACACCACTGAGAGCGGCTGAGAGAGGATCCAGAAAGT 900

[illegible]

4141	DB	TTTCAGATGATGAAGAAAGAGGAAACGGGCTTTGGAGAGAAAATAATCAAGAGAGACCAAGACA	4201
4201	QY	TGGATTCAAACTTTAGGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAAGCGTCTCTGAAG	4261
4201	DB	TGGATTCAAACTTTAGGTGAAGACAGCATCTGGGTGTGAGAGTGAACAAAGCGTCTCTGAAG	4260
4261	QY	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCATCAGCAGAGGATACCAATGC	4320
4261	DB	ACTGCTCAGGGCTATCTCTCAGAGTGACATTTTAAACCATCAGCAGAGGATACCAATGC	4320
4321	QY	AACATAACCTGTATAAAGCTCCAGCAGGAAATGGCTGAACATAGAGCTGTGTATGAACAGC	4380
4321	DB	AACATAACCTGTATAAAGCTCCAGCAGGAAATGGCTGAACATAGAGCTGTGTATGAACAGC	4380
4381	QY	ATGGAGCGAGCCCTCTTAAACAGCTACCCCTCCATCATTAAGTGACTCTTCTGCGCTTGAGG	4440
4381	DB	ATGGAGCGAGCCCTCTTAAACAGCTACCCCTCCATCATTAAGTGACTCTTCTGCGCTTGAGG	4440
4441	QY	ACCTGCCAAATCCAGAAACAAAGCACATCAGAAAAAGCAGTATTAACTTCACAGAAAAGTA	4500
4441	DB	ACCTGCCAAATCCAGAAACAAAGCACATCAGAAAAAGCAGTATTAACTTCACAGAAAAGTA	4500
4501	QY	GTGAATACCTTATAGCCAGATCCAGAGGCGCTTTCTGTGTGACAGATTTGAGGTGTCTG	4560
4501	DB	GTGAATACCTTATAGCCAGATCCAGAGGCGCTTTCTGTGTGACAGATTTGAGGTGTCTG	4560
4561	QY	CAGATAGTCTTACAGTAAAAATAAAGAACAGAGGTGGAAGGTCACTCCCTTCTTAAAT	4620
4561	DB	CAGATAGTCTTACAGTAAAAATAAAGAACAGAGGTGGAAGGTCACTCCCTTCTTAAAT	4620
4621	QY	GCCCATCAITTAGATGATAGTGGGTACATGACAGTTGCTCTGGAGTCTTCAGAAATAGAA	4680
4621	DB	GCCCATCAITTAGATGATAGTGGGTACATGACAGTTGCTCTGGAGTCTTCAGAAATAGAA	4680
4681	QY	ACTACCCATCTCAGAGGAGGTCAITTAAGGTGTGTGATGTGGAGGACACAGCTGGAAG	4740
4681	DB	ACTACCCATCTCAGAGGAGGTCAITTAAGGTGTGTGATGTGGAGGACACAGCTGGAAG	4740
4741	QY	AGTCTGGGCCACACGATTTGACGGAAACATCTTTACTTTGCCAAGCCAGATCTTAGAGGGAA	4800
4741	DB	AGTCTGGGCCACACGATTTGACGGAAACATCTTTACTTTGCCAAGCCAGATCTTAGAGGGAA	4800
4801	QY	CCCCTTACCTTGGAACTGTGGAAATCAGCGCTTCTCTGTATGACCCGTGAATCTGTCTCTG	4860
4801	DB	CCCCTTACCTTGGAACTGTGGAAATCAGCGCTTCTCTGTATGACCCGTGAATCTGTCTCTG	4860
4861	QY	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATACCATCTTCAACTCTGTGATTTGA	4920
4861	DB	AAGACAGAGCCCCAGAGTCAAGTCTGTGTGGCAACATACCATCTTCAACTCTGTGATTTGA	4920
4921	QY	AAGTTCCTCCCAATTGAAAGTTGCAGAAATCTGCCCAGAGTCCAGCTGTGCTCATCTACTG	4980
4921	DB	AAGTTCCTCCCAATTGAAAGTTGCAGAAATCTGCCCAGAGTCCAGCTGTGCTCATCTACTG	4980
4981	QY	ATATCTGCTGGTATATGCAATCGAATCGAAGTGTGTGAGCAGGGAGAGCCAGAAFTGCACAG	5040
4981	DB	ATATCTGCTGGTATATGCAATCGAAGTGTGTGAGCAGGGAGAGCCAGAAFTGCACAG	5040
5041	QY	CTTCAAACAGAAAGGGTCAAACAAAGAAATGTCCATGTGTGTGTCTGGCGCTGACCCAGAG	5100
5041	DB	CTTCAAACAGAAAGGGTCAAACAAAGAAATGTCCATGTGTGTGTCTGGCGCTGACCCAGAG	5100
5101	QY	AATTTATGCTGTGTATCAAGTTTGCAGAAAAACACACATCTTAATCTTAATTTA	5160
5101	DB	AATTTATGCTGTGTATCAAGTTTGCAGAAAAACACACATCTTAATCTTAATTTA	5160
5161	QY	CTGAAGAGACTACTCATGTTGTTTATGAAACACATGCTGAGTTGTGTGTGAACGACAC	5220
5161	DB	CTGAAGAGACTACTCATGTTGTTTATGAAACACATGCTGAGTTGTGTGTGAACGACAC	5220
5221	QY	TGAAATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280
5221	DB	TGAAATATTTTCTAGGAATTCGGGAGGAAAAATGGGTAGTTAGCTATTTCTGGGTGACCC	5280

QY 5281 AGTCTATTAAAGAAAGAAATCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340
DB 5281 AGTCTATTAAAGAAAGAAATCTGAATGAGCATGATTTTGAAGTCAGAGGAGATGTGG 5340
QY 5341 TCAATGGAAGAAACCAACCAAGGTCCTCAAGGAGCAAGAGATCCAGGACAGAAAGATCT 5400
DB 5341 TCAATGGAAGAAACCAACCAAGGTCCTCAAGGAGCAAGAGATCCAGGACAGAAAGATCT 5400
QY 5401 TCAGGGGGCTAGAAATCTGTTATGAGGAGGCTTCAACCAATGCTGAGGAGCAAGATCTGG 5460
DB 5401 TCAGGGGGCTAGAAATCTGTTATGAGGAGGCTTCAACCAATGCTGAGGAGCAAGATCTGG 5460
QY 5461 AATGGATGTTACAGCTGTGTGCTCTCTGTGTGAGGAGCTTTTATCATTCACCCCTTG 5520
DB 5461 AATGGATGTTACAGCTGTGTGCTCTCTGTGTGAGGAGCTTTTATCATTCACCCCTTG 5520
QY 5521 GCACAGGTGTCACCCCAATTTGTTGTGAGGAGGCTTGTGAGGAGGAGCAAGATGGCT 5580
DB 5521 GCACAGGTGTCACCCCAATTTGTTGTGAGGAGGCTTGTGAGGAGGAGCAAGATGGCT 5580
QY 5581 TCCATGCAATTTGGGAGAGTGTGAGGAGGCTTGTGAGGAGGAGGAGGAGGAGGAGGAG 5640
DB 5581 TCCATGCAATTTGGGAGAGTGTGAGGAGGCTTGTGAGGAGGAGGAGGAGGAGGAGGAG 5640
QY 5641 GGTAGCACTCTACAGTCCAGGAGCTGAGGAGGCTTGTGAGGAGGAGGAGGAGGAGGAG 5700
DB 5641 GGTAGCACTCTACAGTCCAGGAGCTGAGGAGGCTTGTGAGGAGGAGGAGGAGGAGGAG 5700
QY 5701 GCCACTACTGA 5711
DB 5701 GCCACTACTGA 5711

RESULT 14

US-09-753-1
Sequence 1: Application US/0909753
Patent No. 6149903
GENERAL INFORMATION:
APPLICANT: HOLT, JEFFREY T.
APPLICANT: JENSEN, ROY A.
APPLICANT: PAGE, DAVID L.
APPLICANT: KING, MARY-CLAIRE
APPLICANT: SZABO, CSTILA I.
APPLICANT: JETTON, THOMAS L.
APPLICANT: ROBINSON-BENION, CHERYL L.
APPLICANT: THOMPSON, MARILYN E.
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2
TITLE OF INVENTION: PROTEINS AND SCREENING AND THERAPEUTIC METHODS BASED ON
TITLE OF INVENTION: CHARACTERIZED BRCA1 AND BRCA2 PROTEINS.
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIES A. TAYLOR, JR.
STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
CITY: DURHAM
STATE: NORTH CAROLINA
COUNTRY: USA
ZIP: 27707
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 800 kb storage
COMPUTER: IBM PC/XT/AT compatible
OPERATING SYSTEM: Windows 3.1
SOFTWARE: WORD PERFECT 6.1 and ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/099,753
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/603,753
FILING DATE: 20 FEB 1996
APPLICATION NUMBER: U.S. 08/373,799
FILING DATE: 17 JAN 1995

ATTORNEY/AGENT INFORMATION:
NAME: ARIES A. TAYLOR, JR.
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REFERENCE/DOCKET NUMBER: 1242/2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919) 493-8000
TELEFAX: (919) 419-0383
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 5712
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA to mRNA
HYPOTHETICAL: no
ANTI-SENSE: no
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
INDIVIDUAL ISOLATE:
DEVELOPMENTAL STAGE: adult
TISSUE TYPE: female breast
CELL TYPE: ductal carcinoma in situ, invasive
CELL TYPE: breast cancer and normal breast tissue
CELL LINE: not derived from a cell line
ORGANELLE: no
IMMEDIATE SOURCE:
LIBRARY: cDNA library derived from human
CLONE: obtained using published sequence
POSITION IN GENOME:
CHROMOSOME/SEGMENT: unknown
MAP POSITION: unknown
UNITS: unknown
FEATURE:
NAME/KEY: BRCA1
LOCATION: GenBank accession no. U14680
IDENTIFICATION METHOD: microscopically directed
IDENTIFICATION METHOD: sampling and nuclease protection assay
OTHER INFORMATION: gene encoding BRCA1 protein
PUBLICATION INFORMATION:
AUTHORS: Miki, Y., et. al.
TITLE: A strong candidate gene for the breast and
TITLE: ovarian cancer susceptibility gene BRCA1.
JOURNAL: Science
VOLUME: 266
PAGES: 66-71
DATE: 1994
RELEVANT RESIDUES IN SEQ ID NO: 1:
US-09-099-753-1

Query Match 99.8%; Score 5701.4; DB 3; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 1 AGCTGCTGAGACTTCTGAGACCCCGACACAGGCTGTGGGGTTCTCAGATAAATCTGGGCC 60
DB 1 AGCTGCTGAGACTTCTGAGACCCCGACACAGGCTGTGGGGTTCTCAGATAAATCTGGGCC 60
QY 61 CTTGCGCTCAGAGGCTTCCCTCTCTCTGCGTAAAGTTTCATTTGGAACAGAAAGAAA 120
DB 61 CTTGCGCTCAGAGGCTTCCCTCTCTCTGCGTAAAGTTTCATTTGGAACAGAAAGAAA 120
QY 121 TGGATTATCTGCTTCTGCGTTGAAGAGTACAAAATGTCTAATATGCTATGCAAGAAA 180
DB 121 TGGATTATCTGCTTCTGCGTTGAAGAGTACAAAATGTCTAATATGCTATGCAAGAAA 180
QY 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCCCAAAGTGTGACC 240
DB 181 TCTTAGAGTGTCCCATCTGTCTGAGTTGATCAAGAACCTGTCTCCCAAAGTGTGACC 240
QY 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACCAAGAGAAAGGCTTCACAGT 300
DB 241 ACATATTTTGCAGAAATTTTGCATGCTGAACTTCTCAACCAAGAGAAAGGCTTCACAGT 300

QY	301	GTCTTTATGTAAAGATGATATACCCAAAAGGAGCCCTACAGAAGGTACGAGATTTAGTC	360
DB	301	GTCTCTTTATGTAAAGATGATATACCCAAAAGGAGCCCTACAGAAGGTACGAGATTTAGTC	360
QY	361	AAC TTGTTGAAGAGCTATGGAATAATCATTTGTGCTTTTCAGCTTTGACACAGGTTTGAGT	420
DB	361	AAC TTGTTGAAGAGCTATGGAATAATCATTTGTGCTTTTCAGCTTTGACACAGGTTTGAGT	420
QY	421	ATGCAAAACAGCTATAAATTTTTCGAAAAAGGAAAAATACTCTCTCGAACTCTAAAGATG	480
DB	421	ATGCAAAACAGCTATAAATTTTTCGAAAAAGGAAAAATACTCTCTCGAACTCTAAAGATG	480
QY	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG	540
DB	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGAGTG	540
QY	541	AACCCGAAAAATCCTTCTCTGTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAAACCTTGAA	600
DB	541	AACCCGAAAAATCCTTCTCTGTCAGGAAACCAAGTCTCAGTGTCCAACTCTCTAAACCTTGAA	600
QY	601	CTGTGAGAACTCTGAGGACCAAGCAGCGGTACAACTCCTCAAAAGAGCTCTGTCTACATTG	660
DB	601	CTGTGAGAACTCTGAGGACCAAGCAGCGGTACAACTCCTCAAAAGAGCTCTGTCTACATTG	660
QY	661	AATTTGGGATCTGATTTCTTCTGAAGTACCGTTTAATAGGCAACTTTATGTCAGTGTGGGAG	720
DB	661	AATTTGGGATCTGATTTCTTCTGAAGTACCGTTTAATAGGCAACTTTATGTCAGTGTGGGAG	720
QY	721	ATCAAGAAATTTGTAACAATCAACCCCTCAAGGAAACAGGGATGAAATCAGTTTGTGATTCGT	780
DB	721	ATCAAGAAATTTGTAACAATCAACCCCTCAAGGAAACAGGGATGAAATCAGTTTGTGATTCGT	780
QY	781	CAAAAAAGGCTCTGTTGTGAATTTCTCGAGCGGATGTAAACAAATPACTGAACTCATCAAC	840
DB	781	CAAAAAAGGCTCTGTTGTGAATTTCTCGAGCGGATGTAAACAAATPACTGAACTCATCAAC	840
QY	841	CCAGTAATTAATGATTTGTAACCACTGAGAACCGTGCAGCTGAGAGCATCCAGAAAAGT	900
DB	841	CCAGTAATTAATGATTTGTAACCACTGAGAACCGTGCAGCTGAGAGCATCCAGAAAAGT	900
QY	901	ATCAGGGTAGTCTTGTTTCAAACTTGATGTGGAGCCATGTGGCACAATACTCATGCCCCA	960
DB	901	ATCAGGGTAGTCTTGTTTCAAACTTGATGTGGAGCCATGTGGCACAATACTCATGCCCCA	960
QY	961	GCTCATTTACGATGAGAACACGACGAGTTTATTACTCACTAAAGACAGAAATGAATGTAGAAA	1020
DB	961	GCTCATTTACGATGAGAACACGACGAGTTTATTACTCACTAAAGACAGAAATGAATGTAGAAA	1020
QY	1021	AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGTGCTTAGCAGAGGCCAATCAACAGAT	1080
DB	1021	AGGCTGAATTTCTGTAATAAAGCAAAACAGCTGTGCTTAGCAGAGGCCAATCAACAGAT	1080
QY	1081	GGGCTGGAAGTAAAGCAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAAGGTAG	1140
DB	1081	GGGCTGGAAGTAAAGCAACATGTAATGATAGGCGGACTCCAGCACAGAAAAAAGGTAG	1140
QY	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAATGGAATAGCAAGAACTGTGCTATGCT	1200
DB	1141	ATCTGAATGCTGATCCCTGTGTGAGAGAAAGAATGGAATAGCAAGAACTGTGCTATGCT	1200
QY	1201	CAGAGAACTCTAGAGATACTGAAGATGTTCTCTTGATTAACACTAAATAGCAGCATTCAGA	1260
DB	1201	CAGAGAACTCTAGAGATACTGAAGATGTTCTCTTGATTAACACTAAATAGCAGCATTCAGA	1260
QY	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAACAACTGTTAGGTTCTGTGATGACTCAATGATG	1320
DB	1261	AAGTTAATGAGTGGTTTTCCAGAAAGTGAACAACTGTTAGGTTCTGTGATGACTCAATGATG	1320
QY	1321	GGGAGCTCGAATCAAAAGTGTGCTGATGTAATGAGCGTTCTTAATAGCGGTAGATG	1380
DB	1321	GGGAGCTCGAATCAAAAGTGTGCTGATGTAATGAGCGTTCTTAATAGCGGTAGATG	1380

QY	1381	AAATATCTGGTGTCTT	CAGAGAAAATAGACTT	ACTGCCAGTGATCTCTCATGAGCCTTTAA	1440
DB	1381	AAATATCTGGTGTCTT	CAGAGAAAATAGACTT	ACTGCCAGTGATCTCTCATGAGCCTTTAA	1440
QY	1441	TATGTAAGAAGTGAAGAGTT	CACTCCAAAATCAGTAGAGAGTAATAT	TGGAAGACAAAATAT	1500
DB	1441	TATGTAAGAAGTGAAGAGTT	CACTCCAAAATCAGTAGAGAGTAATAT	TGGAAGACAAAATAT	1500
QY	1501	TTGGGAAAACTTATCGAAGAGGCAAGCCT	CCCCAACTTAAGCCATGTAACCTGAAAATC	1560	
DB	1501	TTGGGAAAACTTATCGAAGAGGCAAGCCT	CCCCAACTTAAGCCATGTAACCTGAAAATC	1560	
QY	1561	TAATTTATAGGAGCAATTTGTTTACT	GAGGCCACAGATATAACAAGAGCGTCCCT	CACAAAATA	1620
DB	1561	TAATTTATAGGAGCAATTTGTTTACT	GAGGCCACAGATATAACAAGAGCGTCCCT	CACAAAATA	1620
QY	1621	AAITAAAGCGTAAGAAGAGACCT	ACATCAGGCGCTTCATCTCTGAGGATTTTAT	CAAGAAAG	1680
DB	1621	AAITAAAGCGTAAGAAGAGACCT	ACATCAGGCGCTTCATCTCTGAGGATTTTAT	CAAGAAAG	1680
QY	1681	CAGATTTGGCAGTTTCAAAACACT	CTCTGAAATGATAAATCAGGCAACTA	CAACCAAAACGAGC	1740
DB	1681	CAGATTTGGCAGTTTCAAAACACT	CTCTGAAATGATAAATCAGGCAACTA	CAACCAAAACGAGC	1740
QY	1741	AGAAATGGTCAAGTGATGAATAT	TACTAATATAGTGGTCATGTAGAAATAA	CAAAAGGTCATT	1800
DB	1741	AGAAATGGTCAAGTGATGAATAT	TACTAATATAGTGGTCATGTAGAAATAA	CAAAAGGTCATT	1800
QY	1801	CTATTTCAAGATGAGAAAAT	CTTAACCCATAGATCACTCGAAAAGAAAT	CTGCTTTTCA	1860
DB	1801	CTATTTCAAGATGAGAAAAT	CTTAACCCATAGATCACTCGAAAAGAAAT	CTGCTTTTCA	1860
QY	1861	AAACGAAGCTGAACCTTATAAGCAGCAGT	ATAAGCAATATGGAACCTCGAAT	TAATAATCC	1920
DB	1861	AAACGAAGCTGAACCTTATAAGCAGCAGT	ATAAGCAATATGGAACCTCGAAT	TAATAATCC	1920
QY	1921	ACAATTCAAAAGCACCTTAA	AAAGAAATAGGCTTAGAGGGAAGTCTTCT	TAACAGGCATATTC	1980
DB	1921	ACAATTCAAAAGCACCTTAA	AAAGAAATAGGCTTAGAGGGAAGTCTTCT	TAACAGGCATATTC	1980
QY	1981	ATGGCGTTTGAACCTAGTAGT	CAGTAGAAATCTAAGGCCACCTAAT	TGTTACTGAAATTCGAAA	2040
DB	1981	ATGGCGTTTGAACCTAGTAGT	CAGTAGAAATCTAAGGCCACCTAAT	TGTTACTGAAATTCGAAA	2040
QY	2041	TTGATAGTGTCTTAGCAGTGAAGAGATA	AAAGAAAAAAGTAGTACAAACCAAT	GCCAGTCA	2100
DB	2041	TTGATAGTGTCTTAGCAGTGAAGAGATA	AAAGAAAAAAGTAGTACAAACCAAT	GCCAGTCA	2100
QY	2101	GGCACACGAGAAACCTTACAACT	CATCGAAGGTAAGAACTCTGCAACTG	GAGCCCAAGAGA	2160
DB	2101	GGCACACGAGAAACCTTACAACT	CATCGAAGGTAAGAACTCTGCAACTG	GAGCCCAAGAGA	2160
QY	2161	GTAACAAGCCAAATGAAACAGACAAAGT	AAAAAGACATGACAGTGAATCTTCT	CCCCAGAGCTGA	2220
DB	2161	GTAACAAGCCAAATGAAACAGACAAAGT	AAAAAGACATGACAGTGAATCTTCT	CCCCAGAGCTGA	2220
QY	2221	AGTTAAACAATATGCACCTGGTCTT	TCTTACTAAGTGTTCAAATACACAGT	GAACCTTAAGAAT	2280
DB	2221	AGTTAAACAATATGCACCTGGTCTT	TCTTACTAAGTGTTCAAATACACAGT	GAACCTTAAGAAT	2280
QY	2281	TTGTGCAATCTTAGCCTTCCAAAGAGAGAA	AAAAAGAGAACTTAGAAACAGT	TTTAAAGTGT	2340
DB	2281	TTGTGCAATCTTAGCCTTCCAAAGAGAGAA	AAAAAGAGAACTTAGAAACAGT	TTTAAAGTGT	2340
QY	2341	CTAATAATGTGAGAGACCCCAAAGATCT	CAATGTTAAGTGAAGAAAGGTTTTC	CAAACTG	2400
DB	2341	CTAATAATGTGAGAGACCCCAAAGATCT	CAATGTTAAGTGAAGAAAGGTTTTC	CAAACTG	2400
QY	2401	AAAGATCTGTAGAGAGTAGCAGTATTT	CACTGGTACTGTAATATGGCAGCTCAGG	2460	
DB	2401	AAAGATCTGTAGAGAGTAGCAGTATTT	CACTGGTACTGTAATATGGCAGCTCAGG	2460	
QY	2461	AAAGTATCTCGTTACTGGAAGTGTAGCACT	CTAGGGGAAGCCAAACACAGAAACCAAA	TAAAT	2520

Db 2461 AAAGTATCTCGTTACTGGAAGTTAGCACTCTAGGGAAGGCAAAACAGACACCAATATAT 2520
Qy |||||
Db 2521 GTGTGAGTCAGTGTGTCAGCAATTTGAAACCCCAAGGCGTAATTCATGTTGTTCCAAAG 2580
Qy |||||
Db 2521 GTGTGAGTCAGTGTGTCAGCAATTTGAAACCCCAAGGCGTAATTCATGTTGTTCCAAAG 2580
Qy |||||
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RESULT 15
US-08-986-106-1
; Sequence 1, Application us/08986106
; Patent No. 6177410
; GENERAL INFORMATION:
; APPLICANT: HOLT, JEFFREY T.
; APPLICANT: JENSEN, ROY A.
; APPLICANT: KING, MARY-CLAIRE
; APPLICANT: STEINER, MITCHELL S.
; APPLICANT: ROBINSON-BENION, CHERYL L.
; APPLICANT: THOMPSON, MARILYN E.
; TITLE OF INVENTION: THERAPEUTIC METHODS FOR
; TITLE OF INVENTION: PROSTATE CANCER
; NUMBER OF SEQUENCES: 26
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARLES A. TAYLOR, JR.
; STREET: SUITE 1401, UNIVERSITY TOWER, 3100 TOWER
; STREET: BOULEVARD
; CITY: DURHAM
; STATE: NORTH CAROLINA
; COUNTRY: USA
; ZIP: 27707
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44MB storage
; COMPUTER: IBM PC/XT/AT compatible
; OPERATING SYSTEM: Windows 3.1
; SOFTWARE: WORD PERFECT 6.1 and ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/986,106
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/603,753
; FILING DATE: 20 FEB 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: ARLES A. TAYLOR, JR.
; REGISTRATION NUMBER: 39,395
; REFERENCE/DOCKET NUMBER: 1242/3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 493-8000
; TELEFAX: (919) 419-0383
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5712
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: BRCA1
; LOCATION: GenBank accession no. U14680
; PUBLICATION INFORMATION:
; AUTHORS: Miki, Y., et. al.
; TITLE: A strong candidate gene for the breast and
; TITLE: ovarian cancer susceptibility gene BRCA1.
; JOURNAL: Science
; VOLUME: 266
; PAGES: 66-71
; DATE: 1994
US-08-986-106-1

Query Match 99.8%; Score 5701.4; DB 3; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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3301 TAGGTTCCAGTGTAGAAACATTTCAAGCAGAACTAGGTAGAAACAGAGGGCCAAAATTGA 3360 Qy
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3361 ATGCTATGCTTAGATTAGGGGTTTTCGAACTGAGTCTATATAAATAAGTCTTCTCTGGAA 3420 Qy
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3661 TCCAGAGAGGAGAGTCTAGCAGGAGTCTGACCCCTTTTCCACCATACACATTTGGCTCAGG 3720 Qy
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Search completed: June 12, 2004, 06:34:23
Job time : 383 secs

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OM nucleic - nucleic search, using sw model

Run on: June 11, 2004, 18:22:53 ; Search time 21381 Seconds
(without alignments)
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Title: US-09-734-672A-3

Perfect score: 5711
Sequence: 1 AGTCGCTGAGACTTCTGCG.....TCCCCCAGACCACTACTGA 5711

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 1: gb_ba.*
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- 3: gb_in.*
- 4: gb_lm.*
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- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	5709.4	100.0	5711	6	AR112808	Sequence AR112808
5	5709.4	100.0	5711	6	I59546	Sequence I59546
6	5703	99.9	5711	6	AR007334	Sequence AR007334
7	5703	99.9	5711	6	AR112810	Sequence AR112810
8	5701.4	99.8	5711	6	AR033056	Sequence AR033056
9	5701.4	99.8	5711	6	AX659576	Sequence AX659576
10	5701.4	99.8	5711	9	HSU14680	Sequence HSU14680
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15	5701.4	99.8	5914	6	AR004673	Sequence AR004673
16	5701.4	99.8	5914	6	AR008159	Sequence AR008159
17	5701.4	99.8	5914	6	AR136942	Sequence AR136942
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ALIGNMENTS

RESULT 1	AR007335	AR007335	5711 bp	DNA	linear	PAT 04-DEC-1998
LOCUS	Sequence 5	from patent US 5750400.				
DEFINITION	AR007335					
ACCESSION	AR007335	GI:3966819				
VERSION	AR007335.1					
KEYWORDS	Unknown.					
SOURCE	Unknown.					
ORGANISM	Unclassified.					
REFERENCE	1 (bases 1 to 5711)					
AUTHORS	Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J., Schelker, D.B. and Zeng, B.					
TITLE	Coding sequences of the human BRCA1 gene					
JOURNAL	Patent: US 5750400-A 5 12-MAY-1998;					

FEATURES		Location/Qualifiers	
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		/mol_type="unassigned DNA"	
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Query Match		100.0%;	Score 5711; DB 6; Length 5711;
Best Local Similarity		100.0%;	Pred. No. 0;
Matches 5711; Conservative		0;	Mismatches 0; Indels 0; Gaps 0;
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Dd	1	AGCTGGCTGAGATCTCTGGACCCGACACAGGCTGGGGTTCTCAGATAAATCTGGGCC	60
Qy	61	CCTGGCTCAGAGGCTTCAACCTCTGCTCTGGTAAAGTTCAATGGAAACAGAAAGAA	120
Dd	61	CCTGGCTCAGAGGCTTCAACCTCTGCTCTGGTAAAGTTCAATGGAAACAGAAAGAA	120
Qy	121	TGGATTTATCTGCTCTCTGGCTTGAAGAGTACAAATGTCAATTAATGCTATGAGAAA	180
Dd	121	TGGATTTATCTGCTCTCTGGCTTGAAGAGTACAAATGTCAATTAATGCTATGAGAAA	180
Qy	181	TCCTAGAGTCCCATCTGCTGGAGTTGATCAAGGACCTGTCTCCACAAGGTGACCC	240
Dd	181	TCCTAGAGTCCCATCTGCTGGAGTTGATCAAGGACCTGTCTCCACAAGGTGACCC	240
Qy	241	ACATATTTGCAAAATTTTGCATGCTGAAATCTTCAACCAAGAGAAAGGGGCTTCAAGT	300
Dd	241	ACATATTTGCAAAATTTTGCATGCTGAAATCTTCAACCAAGAGAAAGGGGCTTCAAGT	300
Qy	301	GTCTTATGTAAGATGATATACCAAAAGGAGCTACAGAAAGTACGAGATTTAGTC	360
Dd	301	GTCTTATGTAAGATGATATACCAAAAGGAGCTACAGAAAGTACGAGATTTAGTC	360
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Dd	481	AAGTTCTATCATCAAAAGTGGCTACAGAAACCGTCCAAAGAGCTTCTACAGAGTG	540
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Dd	781	CAAAAGAGCTCTGAGTGAATTTCTGAGACCGATGTAACAAATCTGATCAATCAAC	840
Qy	841	CCAGTAATATGATTTGAAACCACTGAGAGAGCTGACAGTCCAGAGGATCCAGAAAGT	900
Dd	841	CCAGTAATATGATTTGAAACCACTGAGAGAGCTGACAGTCCAGAGGATCCAGAAAGT	900
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Dd	1201	CAGAGATCTCTAGAGATCTGAGATGTTCTCTTGGATTAACACTTAATAGCAGCATTCAGA	1260
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Dd	1261	AAGTTAATGAGTGTCTTCCAGAAAGTGAAGAACTGTTAGTCTGATGACTCAATGATG	1320
Qy	1321	GGAGTCTGAAATGCAAAAGTACGATGTTTGGACGTTCTTAAATGAGGTAGATG	1380
Dd	1321	GGAGTCTGAAATGCAAAAGTACGATGTTTGGACGTTCTTAAATGAGGTAGATG	1380
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Dd	1381	AATATTTCTGTTCTTCCAGAGAAATAGACTTACTGCGCAGTGTATCTCATGAGGCTTTAA	1440
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Dd	1441	TATGTAAGTGAAGAGTCTCTCAAAATCAGTAGAGATTAATTTGAAGACAAATAT	1500
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Dd	1921	ACAAATCAAAAGCCTTAAAGAAATAGGCTGAGGAGGAGTCTTCTACAGGACATATTC	1980
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Qy 2401 AAGATCTGTAGAGAGTACAGTATTTCACTGTACCTGTGTAATGAGAGAGGTTTGCAGACTG 2460
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Qy 2941 ATGCCAAATGTAGTATCAAGAGGCTCTAGGTTTGTCTATCATCTCAGTTTCAGAGGCA 3000
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Db 3121 AAAACTTTGAGGAACTTCAATGTCACTGAAAGAGAAATGGAAATGAGAACTTCCAA 3180
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Qy 3781 AAGAGCTTCCCTGCTTCCAAACACTGTTATTTGGTAAAGTAAACATATACCTTCTCAGT 3840
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Db |||||
Qy 4141 TTTTCAAGTATGAAGAAAGAGGAAACGGGCTTGGAAAGAAATTAATCAAGAGAGAGCAAGCA 4200
Db |||||
Qy 4201 TGGATTCAAACTTAGGTGAAGAGAGTCTGGGTGTGAGTGAAGTGAAGTGAAGTGAAGTGAAG 4260
Db |||||

DB 241 ACATATTTTGCATCTGGAACCTTCTCAACAGAAAGAGGCGCTTCCACAGT 300
QY 301 GTCCCTTTATGTAAGATGATATAACCAAGAGAGGCTTACAGAAAGTAGGAGATTAGTC 360
DB 301 GTCCCTTTATGTAAGATGATATAACCAAGAGAGGCTTACAGAAAGTAGGAGATTAGTC 360
QY 361 AACTTGTGAGAGACTATGGAATCAATTTGCTTTTTCAGCTTGCACACAGGTTTGGAGT 420
DB 361 AACTTGTGAGAGACTATGGAATCAATTTGCTTTTTCAGCTTGCACACAGGTTTGGAGT 420
QY 421 ATGCAAAAGCTATATTTTGCAGAAAGGAAATTAACCTCTCTGAAACATCTTAAAGATG 480
DB 421 ATGCAAAAGCTATATTTTGCAGAAAGGAAATTAACCTCTCTGAAACATCTTAAAGATG 480
QY 481 AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGT 540
DB 481 AAGTTTCTATCATCAAAAGTATGGGCTACAGAAACCGTGCAGAAAGCTTCTACAGAGT 540
QY 541 AACCCGAAATCTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
DB 541 AACCCGAAATCTCTCTGAGGAAACCAAGTCTCAGTGTCCAACTCTCTAACCTTGGAA 600
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DB 601 CTGTGAGAACTCTGAGGACAAAGCGCGGATACAACTCAAGAGCGTCTGTCTACATG 660
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DB 661 AATTTGGATCTGATTTCTGGAAGATACCGTTAATAAGGCACTTATTGCGAGTGGAG 720
QY 721 ATCAAGAAATGTTTCAAAATCACCCCTCAAGGACCAAGGATGAATCAAGTATGATCTG 780
DB 721 ATCAAGAAATGTTTCAAAATCACCCCTCAAGGACCAAGGATGAATCAAGTATGATCTG 780
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DB 781 CAAAAGGCTCTGTGAAATTTCTGAGCGGATGAACCAATCAATCAATCAATCAATCAAC 840
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DB 841 CCAGTAATATGATTTGAACACCACTGAGGACCGTGCAGCTCAGAGGSCATCCAGAAAGT 900
QY 901 ATCAGGATGATTTCTGTTTCAAACTTGATGTGGAGCCATGTGCAAAATCTCATGCA 960
DB 901 ATCAGGATGATTTCTGTTTCAAACTTGATGTGGAGCCATGTGCAAAATCTCATGCA 960
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DB 961 GCTCATTAAGCATGAGACAGCAGTTTATTAATCACTAAGACAGAAATGAATGTAGAA 1020
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DB 1021 AGGCTGAATTTCTGTTTAAAGCAACAGCTGCTTAGCAAGGACCAACATACAGAT 1080
QY 1081 GGGCTGGAAGTAAAGCAACATGATGTAGGCGACTCCAGCAGAGAAAGGAGTAG 1140
DB 1081 GGGCTGGAAGTAAAGCAACATGATGTAGGCGACTCCAGCAGAGAAAGGAGTAG 1140
QY 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGATGGAATAGCAGAACTGCCATCT 1200
DB 1141 ATCTGAATGCTGATCCCTGCTGTGAGAGAAAGATGGAATAGCAGAACTGCCATCT 1200
QY 1201 CAGAGATCTGAGATGATGAGATGTTCTGAGATACATTAATGAGCAGATTCAGA 1260
DB 1201 CAGAGATCTGAGATGATGAGATGTTCTGAGATACATTAATGAGCAGATTCAGA 1260
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DB 1261 AAGTTAATGAGTGGTTTTCAGAGATGATGATGTTTCTGATGACTCAGATGATG 1320
QY 1321 GGGAGTCTGAATCAAAATGCAAGTACTGATGTATTGGAAGCTTCTTAATGAGGTAGT 1380
DB 1321 GGGAGTCTGAATCAAAATGCAAGTACTGATGTATTGGAAGCTTCTTAATGAGGTAGT 1380

QY 1381 AATATTTCTGTTCTTTCAGAGAAATAGACTTATCTGGCCAGTGATCTCTCATGAGGCTTAA 1440
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QY 1441 TATGTAAAGTGAAGAGTTCACCTCCAAATCAGTAGAGAGTAATATTTGAAGACAAATAT 1500
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QY 1561 TAAATTAAGGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCTCAAAATA 1620
DB 1561 TAAATTAAGGAGCAATTTGTTACTGAGCCACAGATAATACAGAGCGTCCCTCTCAAAATA 1620
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DB 1621 AATTAAGCGTAAAGGAGACCTACATCAGGCTTCTATAGGAGATTTTATCAAGAAAG 1680
QY 1681 CAGATTTGGCAGTTTCAAGAGCTCTGAAATGATAAATCAGGAACTAAACCAAGCGAGC 1740
DB 1681 CAGATTTGGCAGTTTCAAGAGCTCTGAAATGATAAATCAGGAACTAAACCAAGCGAGC 1740
QY 1741 AGAATGCTCAAGTGAATATTTACTAATAGTGTCTATAGCAATTAAGCAAAAGGTGAT 1800
DB 1741 AGAATGCTCAAGTGAATATTTACTAATAGTGTCTATAGCAATTAAGCAAAAGGTGAT 1800
QY 1801 CTATTCAGATGAGAAATCTTAAACCAATAGATCACTCGAAAGAGATCTGCTTCA 1860
DB 1801 CTATTCAGATGAGAAATCTTAAACCAATAGATCACTCGAAAGAGATCTGCTTCA 1860
QY 1861 AAAAGGAGTGAACCTTATAGCAGCAGTATAAGCAATATGGAATCGAATTAATATTC 1920
DB 1861 AAAAGGAGTGAACCTTATAGCAGCAGTATAAGCAATATGGAATCGAATTAATATTC 1920
QY 1921 ACAATTAAGACCTTAAAGAAATAGGCTGAGGAGAGTCTTCTACAGGATATTC 1980
DB 1921 ACAATTAAGACCTTAAAGAAATAGGCTGAGGAGAGTCTTCTACAGGATATTC 1980
QY 1981 ATGCGCTGAGTACTAGTACTAGTAGAATCTAAGCCACCTAATTTGACTGAAATGCAAA 2040
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DB 2041 TTGATAGTGTCTTAGCAGTGAAGAGATAAGAAAAAGTACACCAATATGCGAGTCA 2100
QY 2101 GGCAAGCAGAACTTCAACTCATGAAAGTAAAGAACCTGCAACTGGAGCCAGAGAGA 2160
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QY 2161 GTAAAGAGCCAAATGAACAGACAAAGTAAAGACATGACAGTGTACTTCCAGAGCTGA 2220
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DB 2221 AGTTAAAGATGCACTGCTTCTTTACTAGTGTTCAAATACAGTGAATTAAGAT 2280
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DB 2341 CTAAATATGCTGAAGACCCCAAGATCTCATGTTTAACTGAGAAAGGTTTGAAGCTG 2400
QY 2401 AAGATCTGTAGAGAGTAGGATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460
DB 2401 AAGATCTGTAGAGAGTAGGATTTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 2460

Qy	2461	AAAGTATCTCGTTATCTGGAAAGTTAGCACTCTAGGGAAGGCAAAAAAGAAACCAAAATAAAT	2520
Db	2461		2520
Qy	2521	GTGTGAGTCAAGTGTGAGCACTTTGAAAACCCCAAGGCACTAAATCATGGTTGTTCCAAAG	2580
Db	2521		2580
Qy	2581	ATAATGAAATGACACAGAAGGCTTTTAAGTATCCATTGGGACATGAAGTTAACACAGTCT	2640
Db	2581		2640
Qy	2641	GGGAAACACGATAGAAATGCGAGAGTCAACTTGGATGCTCAGTATTTTCGCAATACAT	2700
Db	2641		2700
Qy	2701	TCAGGTTTCAAAGCGCAGTCATTTGCTCTGTGTTTCAAAATCCAGGAAATGCAAGAGG	2760
Db	2701		2760
Qy	2761	AATGTGCAACATTTCTCTGCCCACCTCTGGGTCTTTAAGAAACAAAGTCCAAAAGTCACATT	2820
Db	2761		2820
Qy	2821	TTGAAATGTGAACAAAGCAAGCAAAATCAAGGAAGAAATGAGTCTAATATCAAGCCTGTAC	2880
Db	2821		2880
Qy	2881	AGACAGTTAATATCATCTGCAAGCTTTTCTGTGGTTGTCAGAAAGATTAAGCCAGTTGATA	2940
Db	2881		2940
Qy	2941	ATGCCAAATGTAGTATCAAAAGAGGCTCTAGGTTTCTCTATCATCTCAGTTCAGAGGCA	3000
Db	2941		3000
Qy	3001	ACGAAACTGGACTCATTACTCCAAATAAACATGGACTTTTCAAAAACCCATATCGTATAC	3060
Db	3001		3060
Qy	3061	CACACATTTTCCCATCAAGTCAATTTTAAACTTAACATTAATCTAGAAATAATCTCTAGAGG	3120
Db	3061		3120
Qy	3121	AAAACTTTGAGGAACATTCAAATGTCACTGAAAGAGAAATGGGAAATGAGAAATTTCCAA	3180
Db	3121		3180
Qy	3181	GTAAGTGAAGCAATTAAGCGTAAATTAACATTAAGAGAAATGTTTTTAAAGGAGCCAGCT	3240
Db	3181		3240
Qy	3241	CAAGCAATATTAATGAAGTAGGTTCCAGTACTAATGAAGTGGGCTCCAGTATTAATGAAA	3300
Db	3241		3300
Qy	3301	TAGGTTCCAGTGATGAAACATTCAGCAAGAACTTAGGTAGAAACAGAGGAGCCAAATTTGA	3360
Db	3301		3360
Qy	3361	ATGCTATGCTTAGATTAAGGGTTTTGCAACTGAGGTCTATAAACAAAGTCTTCTCGGAA	3420
Db	3361		3420
Qy	3421	GTAATTTGAGCATCTCGAAATATAAAAGCAAGAAATTAAGAAAGTAGTTTCAGATCTGTTA	3480
Db	3421		3480
Qy	3481	ATACAGATTTCTTCCATATCTGATTTTCAGATTAATCTAGAACAGCCTATCGGAAGTAGTC	3540
Db	3481		3540
Qy	3541	ATGCATCTCAGGTTTTCTTGAGACACCTGTATGACCTGTATGATGATGGTGAATAAAGG	3600

Db	3541		ATGCATCTCAGGTTTGTCTGAGCACCTGATGACCTGTTAGATGATGGTGAATAAAGG	3600
Qy	3601		AAGATACTAGTTTGTCTGAAATGACATTAAGAAAGTTCTGCTGTTTTTGTAGCAAAAGCG	3660
Db	3601		AAGATACTAGTTTGTCTGAAATGACATTAAGAAAGTTCTGCTGTTTTTGTAGCAAAAGCG	3660
Qy	3661		TCAGAGAGAGAGCTTTAGCAGAGGCTCTAGCCCTTTACCCATACACATTTTGGCTCAGG	3720
Db	3661		TCAGAGAGAGAGCTTTAGCAGAGGCTCTAGCCCTTTACCCATACACATTTTGGCTCAGG	3720
Qy	3721		GTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGAACTTATCTAGTGAGGATG	3780
Db	3721		GTTACCGAAGAGGGGCCAAGAAATTAGAGTCCTCAGAAGAACTTATCTAGTGAGGATG	3780
Qy	3781		AAGAGCTTCCTGCTTCCACACCTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
Db	3781		AAGAGCTTCCTGCTTCCACACCTGTTATTTGGTAAAGTAAACAATATACCTTCTCAGT	3840
Qy	3841		CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTTAAGAAACACAGAGGAGAAATTTAT	3900
Db	3841		CTACTAGGCATAGCACCGTTGCTACCGAGTGTCTGTTAAGAAACACAGAGGAGAAATTTAT	3900
Qy	3901		TATCATTTGAAGATAGCTTAAATGACTGTCAGTAAACAGGTAATATTGGCAAGGCATCTC	3960
Db	3901		TATCATTTGAAGATAGCTTAAATGACTGTCAGTAAACAGGTAATATTGGCAAGGCATCTC	3960
Qy	3961		AGGAACATCACCCTTAGTGAGAAACAAAATGTTCTGTAGCTTGTGTTTTTCTTACAGTGCA	4020
Db	3961		AGGAACATCACCCTTAGTGAGAAACAAAATGTTCTGTAGCTTGTGTTTTTCTTACAGTGCA	4020
Qy	4021		GTGAATTTGGAAGACTTGACTGCAAAATCAAAACCCAGAGTCCCTTCTTCAATTGGTCTTT	4080
Db	4021		GTGAATTTGGAAGACTTGACTGCAAAATCAAAACCCAGAGTCCCTTCTTCAATTGGTCTTT	4080
Qy	4081		CCAAACAAATGAGGCATCAGTCTGAAAGCAGGGAGTTGGTCTGAGTGACAAGGAATGG	4140
Db	4081		CCAAACAAATGAGGCATCAGTCTGAAAGCAGGGAGTTGGTCTGAGTGACAAGGAATGG	4140
Qy	4141		TTTCAGATGATGAAGAAAGAGAAACGGCTTTGGAAGAAAATAATCAAGAGAGCAAGACA	4200
Db	4141		TTTCAGATGATGAAGAAAGAGAAACGGCTTTGGAAGAAAATAATCAAGAGAGCAAGACA	4200
Qy	4201		TGGATTTCAACTTAGTTGAAGCAGCATCTGGGTGTGAGGTGGAACAGGCTCTCTGAAG	4260
Db	4201		TGGATTTCAACTTAGTTGAAGCAGCATCTGGGTGTGAGGTGGAACAGGCTCTCTGAAG	4260
Qy	4261		ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCATGC	4320
Db	4261		ACTGCTCAGGCTATCTCTCAGAGTGACATTTTAAACCATCTCAGCAGAGGATACCATGC	4320
Qy	4321		AACATACTGTATAAAGCTCCAGAGAAATGGCTGAACTAGAGCTGTGTTAGAACAGC	4380
Db	4321		AACATACTGTATAAAGCTCCAGAGAAATGGCTGAACTAGAGCTGTGTTAGAACAGC	4380
Qy	4381		ATGGAGCAGCCTTTCTAAACAGCTTACCCTTCCATATAAGTGACTCTTCTGCCCTTCAGG	4440
Db	4381		ATGGAGCAGCCTTTCTAAACAGCTTACCCTTCCATATAAGTGACTCTTCTGCCCTTCAGG	4440
Qy	4441		ACCTTCGAAATTCAGAAACAAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAGTA	4500
Db	4441		ACCTTCGAAATTCAGAAACAAAGCACATCAGAAAAAGCAGTATTAACTTTCACAGAAAGTA	4500
Qy	4501		GTGAAATCCCTATTAAGCCGAAATCCAGAGGCCCTTTCTGCTGACAAGTTTCAGGCTGCTG	4560
Db	4501		GTGAAATCCCTATTAAGCCGAAATCCAGAGGCCCTTTCTGCTGACAAGTTTCAGGCTGCTG	4560
Qy	4561		CAGATAGTTCTTACAGTAAAAATAAGAACCCAGGAGTGGAAAGTGCTATCCCTCTTAAT	4620
Db	4561		CAGATAGTTCTTACAGTAAAAATAAGAACCCAGGAGTGGAAAGTGCTATCCCTCTTAAT	4620
Qy	4621		GCACATCATTTAGTATAGTTGTTACATGCACAGTTCCTCTGGGAGTCTTCAGATAGAA	4680
Db	4621		GCACATCATTTAGTATAGTTGTTACATGCACAGTTCCTCTGGGAGTCTTCAGATAGAA	4680

Db 4621 GCCATCATAGATAGTAGGTGATACATGACAGTTGCTCTGGAGTCTTCAGATAGAA 4680
Qy 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTTGTTGATGTGAGGAGCAACAGCTGGAG 4740
Db 4681 ACTACCCATCTCAAGAGAGCTCATTAAGTTGTTGATGTGAGGAGCAACAGCTGGAG 4740
Qy 4741 AGTCGGGCCACACATTTGACGGAACATCTTACTTCCAGGCAAGATCTAGAGGAA 4800
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Db 4801 CCCCTTACCTGGAATCTGGAATCAGCCTCTCTCTGATGACCCCTGAATCTGATCTTG 4860
Qy 4861 AAGACAGAGCCCGCAGAGTCTGCTGTTGGCAACATACCACTCTCAACCTCTGATGA 4920
Db 4861 AAGACAGAGCCCGCAGAGTCTGCTGTTGGCAACATACCACTCTCAACCTCTGATGA 4920
Qy 4921 AAGTTCCCAATTTGAAAGTTGAGAAATCTGCCAGGCTCCAGCTCTCTCATACTG 4980
Db 4921 AAGTTCCCAATTTGAAAGTTGAGAAATCTGCCAGGCTCCAGCTCTCTCATACTG 4980
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Qy 5101 AATTTATGCTGTGTACAGTTGTCAGAAACACACATCACTTTAATCTAATTA 5160
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Qy 5161 CTGAAGAGACTACTCATGTTGTTATGAACAGATGCTGAGTTGTTGTTGAACCGACAC 5220
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Qy 5221 TGAATATTTCTAGAAATGCGGAGGAAATGSGGTAGTTAGTATTTCTGGGTGACCC 5280
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RESULT 3
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LOCUS
DEFINITION
Sequence 1 from patent US 5750400.
ACCESSION
AR007333
VERSION
AR007333.1 GI:3966817
KEYWORDS
Unknown.
SOURCE
ORGANISM
Unclonable.
REFERENCE
1 (bases 1 to 5711)
MURPHY, D.B., ALLEN, A.C., ALVARES, C.P., CRITZ, B.S., OLSON, S.J.,
SCHEIDER, D.B. and ZENG, B.
TITLE
Coding sequences of the human BRCA1 gene
JOURNAL
Patent: US 5750400-A 1 12-MAY-1998;
FEATURES
Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 5709.4; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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DEFINITION Sequence 1 from patent US 6130322.
ACCESSION AR112808
VERSION AR112808.1 GI:14092708
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,
Thurber, D., and Zeng, B.
TITLE Coding sequences of the human BRCA1 gene
JOURNAL Patent: US 6130322-A 1 10-OCT-2000;
FEATURES Location/Qualifiers
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Query Match 100.0%; Score 5709.4; DB 6; Length 5711;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5710; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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VERSION I59546.1 GI:2478178
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,
Scheller, D.B. and Zeng, B.
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JOURNAL Patent: US 5654155-A 1 05-AUG-1997;
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RESULT 6

AR007334
LOCUS AR007334 5711 bp DNA linear PAT 04-DEC-1998
DEFINITION Sequence 3 from patent US 5750400.
ACCESSION AR007334
VERSION AR007334.1 GI:3966818
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unknown.

Unclassified.									
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Murphy, P.D., Allen, A.C., Alvares, C.P., Critz, B.S., Olson, S.J.,									
Scheller, D.B. and Zeng, B.									
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Query Match 99.9%; Score 5703; DB 6; Length 5711;									
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DEFINITION Sequence 5 from patent US 6130322.
ACCESSION AR112810
VERSION AR112810.1 GI:14092710
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Murphy, P.D., Allen, A.C.P., Alvares, C.P., Critz, B.S., Olson, S.J.,
Thurber, D. and Zeng, B.
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JOURNAL Patent: US 6130322-A 5 10-OCT-2000;
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ORIGIN

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Best Local Similarity 99.9%; Pred. No. 0;
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DB 61 CCTGGCTCAGAGGCGCTTCCACCTCTGCTCTGGTAAAGTTTCATTTGGACACAGAAAGAA 120
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RESULT 8
AR033056 AR033056 5711 bp DNA linear PAT 29-SEP-1999
LOCUS Sequence 1 from patent US 5869245.
DEFINITION AR033056
ACCESSION AR033056
VERSION AR033056.1 GI:5948661
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5711)
AUTHORS Yeung, A.T.
TITLE Mismatch endonuclease and its use in identifying mutations in
targeted polynucleotide strands
JOURNAL Patent: US 5869245-A 1 09-FEB-1999;
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LOCUS	HSU14680	5711 bp	mRNA	linear
DEFINITION	Homo sapiens breast and ovarian cancer susceptibility (BRCA1) mRNA, complete cds.			
ACCESSION	U14680			
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KEYWORDS	Homo sapiens (human)			
SOURCE	Homo sapiens			
ORGANISM	Homo sapiens			
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AUTHORS	Miki,Y., Swensen,J., Shattuck-Eidens,D., Futreal,P.A., Harselman,K., Tavtigian,S., Liu,Q., Cochran,C., Bennett,L.M., Ding,W., Bell,R., Rosenthal,J., Hussey,C., Tran,T., McClure,M., Frye,C., Hattier,T., Phelps,R., Haugen-Strano,A., Katcher,H., Yakumo,K., Gholami,Z., Shaffer,D., Stone,S., Bayer,S., Wray,C., Bogden,R., Dayananth,P., Ward,J., Tonin,P., Narod,S., Bristow,P.K., Norris,F.H., Helvering,L., Morrison,P., Rosteck,P., Lai,M., Barrett,J.C., Lewis,C., Neuhausen,S., Cannon-Albright,L., Goldgar,D., Wiseman,R., Kamb,A. and Skolnick,M.H.			
TITLE	A strong candidate for the breast and ovarian cancer susceptibility gene BRCA1			
JOURNAL	Science	266 (5182), 66-71	(1994)	
MEDLINE	95025896			
PUBMED	7545954			
REFERENCE	2 (bases 1 to 5711)			
AUTHORS	Skolnick,M.H.			
TITLE	Direct Submission			
JOURNAL	Submitted (14-SEP-1994) Mark H. Skolnick, Myriad Genetics Inc. and the University of Utah, 421 Wakara Way, Suite 201, Salt Lake City, UT 84108, USA			
FEATURES	Location/Qualifiers			
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ORIGIN

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RESULT 11

AR070223
LOCUS 5712 bp DNA linear PAT 18-FEB-2000
DEFINITION Sequence 1 from patent US 5891857.
ACCESSION AR070223
VERSION AR070223.1 GI:7221111
KEYWORDS Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 5712)
AUTHORS Holt, J.T., Jensen, R.A., King, M.-C., Page, D.L., Szabo, C.I.,
Jeton, T.L., Robinson-Benion, C.L. and Thompson, M.E.
TITLE Characterized BRCA1 and BRCA2 proteins and screening and
therapeutic methods based on characterized BRCA1 and BRCA2 proteins
JOURNAL Patent: US 5891857-A 1 06-APR-1999;
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/organism="unknown"
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ORIGIN

Query Match 99.8%; Score 5701.4; DB 6; Length 5712;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 5705; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

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Db	1	AGCTCGCTGAGACTTCCTGGACCCCGCACCGAGCTGGGGTTCCTCAGATAACTGGGCC	60
Qy	61	CCTGGCTCAGAGAGCCCTTCACTCTGCTCTGGGTAAGTTCATTGGCAACAGAAAGAA	120
Db	61	CCTGGCTCAGAGAGCCCTTCACTCTGCTCTGGGTAAGTTCATTGGCAACAGAAAGAA	120
Qy	121	TGGATTATCTGCTCTTCGGGTTGAAGAGTACAAATGTCAATTAATGCTATGCAGAAA	180
Db	121	TGGATTATCTGCTCTTCGGGTTGAAGAGTACAAATGTCAATTAATGCTATGCAGAAA	180
Qy	181	TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	240
Db	181	TCTTAGAGTGTCCCATCTGCTGGAGTTGATCAAGGAACCTGTCTCCACAAAGTGTGACC	240
Qy	241	ACATATTTGCAATTTTGGATGTGAACTTCTCAACCAAGAAAGGGCTTTCACAGT	300
Db	241	ACATATTTGCAATTTTGGATGTGAACTTCTCAACCAAGAAAGGGCTTTCACAGT	300
Qy	301	GTCCCTTATGTAAGATCATATACCAAGAGGCTTACAGAAAGTACGAGATTAGTC	360
Db	301	GTCCCTTATGTAAGATCATATACCAAGAGGCTTACAGAAAGTACGAGATTAGTC	360
Qy	361	AACCTTTGTTGAAGAGCTATTGAAATCAITTTGCTTTTTCAGCTTGCACAGTTTGGAGT	420
Db	361	AACCTTTGTTGAAGAGCTATTGAAATCAITTTGCTTTTTCAGCTTGCACAGTTTGGAGT	420
Qy	421	ATGCAACAGCTATATTTTGCAAAAGGAAATTAATCTCTCTGACATCTTAAAGATG	480
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Qy	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGATG	540
Db	481	AAGTTTCTATCATCCAAAGTATGGCTACAGAAACCGTGCACAAAGACTTCTACAGATG	540
Qy	541	AACCGGAAATCTCTCTGAGGAAACCACTCTCAGTGTCCAACTCTCTTAACTTGGAA	600
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Qy	601	CTGTGAGAACTCTGAGCAAGACGCGATACAACTTCAAGACGCTCTGTCTACATTG	660
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Qy	661	AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTGCAAGTGGAG	720
Db	661	AATTGGGATCTGATTTCTTCAAGATACCGTTAATAAGGCAACTTATTGCAAGTGGAG	720
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Qy	781	CAAAAAAGGCTGCTGTGAAATTTCTGAGACGGATGTAAACAAATACTGAACATCAAC	840
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Qy	841	CCAGTAATAATGATTTTCAACACCACTGAGAAGCGTGCAGCTGAGAGGCATCCAGAAAAGT	900
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Qy	901	ATCAGGGTAGTCTTCTTTCAAACTTGATGAGAGCCATGTGGCACAATACTCATGCCA	960
Db	901	ATCAGGGTAGTCTTCTTTCAAACTTGATGAGAGCCATGTGGCACAATACTCATGCCA	960
Qy	961	GCTCATTTACAGATGAGAACAGCAGTTTATTTACTTCACTAAAGACAGAAATGAATCTAGAAA	1020
Db	961	GCTCATTTACAGATGAGAACAGCAGTTTATTTACTTCACTAAAGACAGAAATGAATCTAGAAA	1020
Qy	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCTTGGCTTAGCAAGAGCCAACTAACAGAT	1080
Db	1021	AGGCTGAATTTCTGTAATAAAGCAACAGCTTGGCTTAGCAAGAGCCAACTAACAGAT	1080
Qy	1081	GGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCAGCACAAGAAAAGGTAG	1140
Db	1081	GGGCTGGAAGTAAAGGAAACATGTAATGATAGGCGGACTCCAGCACAAGAAAAGGTAG	1140
Qy	1141	ATCTGAATGCTGATCCCTCTGTGAGAGAAAAGAAATGGAATTAAGCAGAACTGCGCATGCT	1200
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Qy	1201	CAGAGATCCTAGAGATACCTGAAGATGTTCTTTGGATTAACACTTAANTAGCAGCAATCAGA	1260
Db	1201	CAGAGATCCTAGAGATACCTGAAGATGTTCTTTGGATTAACACTTAANTAGCAGCAATCAGA	1260
Qy	1261	AAGTTAATGAGTGGTTTCCAGAAAGTGAATGAACTTTAGGTCTCTGATGACTCACATGATG	1320
Db	1261	AAGTTAATGAGTGGTTTCCAGAAAGTGAATGAACTTTAGGTCTCTGATGACTCACATGATG	1320
Qy	1321	GGGAGTCTGAATCAATGCCAAAGTAGCTGATGTAATGGAGCTTTCTAAATGAGGTAGATG	1380
Db	1321	GGGAGTCTGAATCAATGCCAAAGTAGCTGATGTAATGGAGCTTTCTAAATGAGGTAGATG	1380
Qy	1381	AATATTCTGCTTCTTCCAGAGAAAATGACTTCTTGGCCAGTGTATCTCATGAGGCTTTAA	1440
Db	1381	AATATTCTGCTTCTTCCAGAGAAAATGACTTCTTGGCCAGTGTATCTCATGAGGCTTTAA	1440
Qy	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGAAGACAAAATAT	1500
Db	1441	TATGTAAAGTGAAGAGTTCACTCCAAATCAGTAGAGATTAATATTGAAGACAAAATAT	1500
Qy	1501	TTGGGAAACCTATCGGAAAGGAGCGCTCCCACTTAAGCCATGTAACCTGAAATC	1560
Db	1501	TTGGGAAACCTATCGGAAAGGAGCGCTCCCACTTAAGCCATGTAACCTGAAATC	1560
Qy	1561	TAATTATAGGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAATA	1620
Db	1561	TAATTATAGGAGCATTTGTTTACTGAGCCACAGATAATACAAGAGCGTCCCTCACAATA	1620
Qy	1621	AATTAAAGGTAAAGAGACCTTACATCAGGCTTCTATCTCTGAGGATTTTATCAGAAAG	1680
Db	1621	AATTAAAGGTAAAGAGACCTTACATCAGGCTTCTATCTCTGAGGATTTTATCAGAAAG	1680
Qy	1681	CAGATTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAAGGAACTTAACCAACCGGAGC	1740
Db	1681	CAGATTGGCAGTTCAAAAGACTCTCTGAAATGATAAATCAAGGAACTTAACCAACCGGAGC	1740
Qy	1741	AGAATGGTCAAGTGAATGAATTAATTAATAGTGGTCAATGAGATAAATAAAGGTTGAT	1800
Db	1741	AGAATGGTCAAGTGAATGAATTAATTAATAGTGGTCAATGAGATAAATAAAGGTTGAT	1800
Qy	1801	CTATTGAGATGAGAAAATCTTAACCAATCAATCACTCGAAAAGAGATCTGCTTTCA	1860
Db	1801	CTATTGAGATGAGAAAATCTTAACCAATCAATCACTCGAAAAGAGATCTGCTTTCA	1860
Qy	1861	AAACGAAGCTGAACCTATAGCAGCAGTATTAAGCAATATGGAACCTCGAATTAATATCC	1920
Db	1861	AAACGAAGCTGAACCTATAGCAGCAGTATTAAGCAATATGGAACCTCGAATTAATATCC	1920